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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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Li,Z., Morell,M. and Rahman,S. Regulation of gene expression in
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AF064562 Hordeum v
AR340173 Sequence
U66376 Triticum ae
BT008928 Triticum
AF338432 Triticum
AF338432 Triticum
AF26319 Triticum
AF064560 Hordeum v
AY357072 Triticum
AY357072 Triticum
AL731641 Oryza sat
B14724 Rice mRNA f
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AX654742 Sequence
AX755783 Sequence
AR427891 Sequence
AR427891 Sequence
AF064561 Hordeum v
U65948 Zea mays st
AF064563 Hordeum v
E08183 Gene mays
D16201 Oryza sativ
E08183 Gene mays
AF235303 Zea mays
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Minimum Maximum

Qy 661 AGAGACACTTGGCAAGTCCGGCGCAAGCTGAAGAATTACAGGTACACACAC		Qy 421 CTGAACCTGTATTTTTCCCCCCGCGGGGAAATGCGTTAGTGTCACCCAGGCCCTGGTGTT 480	Qy 301 CTCCCCGTCTGGCTTTGGCTCCCTTCTCTCTCTCTGCGCGCGCATGGCCTGTTCAAT 360	Qy 181 GTGTGGCGCGGGCGTCGGAATTGGCGCGGCCGGCTCGGAGCGGAGGGCGAGGGCGG 240 [Best Local Similarity 100.0%; Fred. No. 0; Gaps Matches 2147; Conservative 0; Mismatches 0; Indels 0; Gaps 1 GGCCAGCTTCCACCCCGCGCGCACACGTTGCTCCATCGCTTCTCAATTAATA	II GENE" 100.0%; Score 2147; DB 6; I	source 11.1463 /organism="Aegilops tauschii" /mol_type="unassigned_DNA" /db_xref="taxon:37682" /tisue_type="ENDOSPERM" misc_feature 111463 /product="COMPLETE_SEQUENCE_OF_THE_STARCH_BRANCHING_ENZYME	Patent: WO 99 GOODMAN FIELD RAHMAN SADEQU ORG (AU) ; GR
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Qy 840 TIGITAGCCTIGGCCCCGTGCTGGCTCTTGGGCCACTGAAAAAATCAGATGGATG	EYKRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYKMAAFGAHSAALVGJENNWWF NADTWTRDDYGVWEIFLPNNADGSSAIPHGSRVKIRMDTDSGVKDSISAWIKFSVQAP GEIPFNGIYYDPPEEEKYVFQHPQRKRPESLRIYESHIGMSSPEPKINSYANFRDEVL	
Oy 780 TGCGTCAGGTTTCGAGCTTCTTCTATCAGCATTGTGCAGTACTGCACTGCCTTGTTCATT 8	/ dd xter="91:14" / 30" /translation="MATFAVSGATLGVARAGVGVARAGSERRGGADLPSLLLRKKDSS RAVLSRAASPGKVLVPDGESDDLASPAQPEELQIPEDIEEQTAEVNMTGGTAEKLQSS EPTQGIVETITDGVTKGVKELVVGEKPRVVPKPGDGQKIYEIDPTLKDFRSHLDXRYS	
	/ NOCE SHALLA /codon_start=1 /product="starch branching enzyme IIa" /protein_id="AAK56821.l"	
	2949. 2991,3144. 3203,3539. 3619,3703. 3819,4109. 4109	
Qy 601 TTGCAGGCGCCTCCTGAGCCGCGCCTCTCCAGGGAAGGTCCTGGTGCCTGACGGG 6	12779,	CDS
	7.010.000000000000000000000000000000000	mRNA
1478 CTGAACCTGTATTTTTCCCCCGCGGGGAAATGCGTTAGTGTCACCCAGGCCCTGGTGTT	Shomitted (18-0AN-2001) Figure Industry, Carry, Crumted Canberra, ACT 2601, Australia Location/Qualifiers	FEATURES
	1 to 11475) Regina, A., Li, Z., Sharon, A. and Morell, M.K. mission	PUBMED REFERENCE AUTHORS TITLE
1358	Plant Physiol. 125 (3), 1314-1324 (2001) 21140316	JOURNAL
	relationships among isoforms. Characterization of a gene for starch-branching enzyme IIa from the wheat genome donor Aegilops tanochin	
Qy 241 ACTIGCCGTGCTCCTCAGGAAGAAGACTCCTCTCGTACGCCTCGCTCTCTGAAT 30	Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M., Kosar-Hashemi,B., Abrahams,S. and Morell,M.K. Comparison of starch-branching enzyme genes reveals evolutionary	AUTHORS TITLE
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121	447949	ACCESSION VERSION
Qy 61 TCTCCATCACTCGGGTTCCGCGCTGCATTTCGGCCGGGGGGTTGAGTGAG		RESULT 2 AF338431 LOCUS
QY 1 CGCCAGCTTCCACCCCGGCGCACACGTTGCTCCCCCTTCTCATCGCTTCTCAATTAATA 60	>	
Query Match 98.9%; Score 2124; DB 8; Length 11475; Best Local Similarity 99.9%; Pred. No. 0; Matches 2146; Conservative 0; Mismatches 0; Indels 2; Gaps	3098 ACCAGTTACTATAAATTTATGATCTGGCTTTTGCACCCTGTTACAGTCTGCAGCATTAGT 3157 2101 AGGTGACTTCAACAATTGGAATCCAAATGCAGAATACTATGACCAGAG 2147	0b 3
ORIGIN	2041 ACCAGTTACTATAAATTTATGATCTGGCTTTTGCACCCTGTTACAGTCTGCAGCATTAGT 2100	Ωу 2:
GIALHKMIRLVTMGL/GEGYLUFMGMEFGHEMIDFPRGFQTLDTGKVL/FGNNUSY CRRRFDLGADFLRYRGMQEFDQAMQHLEEKYGFMTSEHQYVSRKHEEDKVIILKR LVFFVRHMSNSFFDYRVGCSKPGKYKVALDSDDALFGGFSRLDHDVDYFTTEHFH RPRSFSVYTPSRTAVVYALTE"	81 TRAITGGTCACTATTCACCAACTAGCTTACTGGACTTACAAATTAGCTTACTGAATACTG 2040 	Qу 198 Db 303
VIMDIVHSISSNNTIDGIUHIY KHGEKKGHMMMUSKKKNI KGSKEVIKK NARWILEEYKFORFREDGVTSMYTHHGILQMTETGNYGEYFGRATUULAVVYIKIU LIHGLYPDAVSIGERVEGGRETECI PVPDGGVGFDYRLHMAVADKWIELLKQSDESW GDIVHTITNRRWILEKCVTYAESHDQALVGDKTIAFWIMDKDMYDGFMALDRESTIRI	921 TCCCTGGAGCGCATGTTATGTTCTTTTAAGTTCCTTAACGAGACACCTTCCAATTTATTG 1980 	Qу 1: Db 2:

PRIKRLGYNAVQIMAIQEHSYYASEGYHVTNEFAPSSREGTEEDLKSLIDRAHELGLL VLMDIVHSHSSNNTLDGLNGFDGTDCTHY EHGGPRGHHWWWDSELFNYGSNEDVLREFLLS NARWHLEEYKFDGFREDGVTSMMYTHHGLQMTETGNYGEYFGEATDVDAVVYLMLVND LIHGLYEDAVSIGEDVGGNFTECIE TVPDGGVYGFDYRLHMAVADKWIELLKOSDESWKW GDIVHTLTNRRWLEKCVTYAESHDQALVGDKTIAFWLMDKDMYDFWALDRESTLRIDR GIALHKMIRLVTWGLIGGEGYLNFWGNEFGHEBWIDF PRGFQTLFTGKVLFGNNNSYDFKREHKMIRLVTWGLIGGEGYLNFWGNEFGHEBWIDF PRGFQTLFTGKVLFGNNNSYDK CRRREDLGDADFLRYEGMEDQAMQHLEKKYGFMTSBHQVUSRKHEEDKVIIKKGD LVFVENFHWSNSFEDKVICKFGKKYKVALDSDDALFGGFSRLDHDVDYFTTEHPHDN RPRSFSVYTPSRTAVVYALTE"

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/translation="MAEVNWTGGAAEKLESSEPTQGIAETITDGVTKGVKELVVGEKP QVVPKPGGQKIXEIDPTLKDFRSHLDYRYSEYK" intron 14351836 /gene="sbelia" exon 1837>1852 /gene="sbelia"		CAAT_signal 719722 /gene="sbella" TATA_signal 727730 /gene="sbella" join(7641434,1837>1852) /gene="sbella" /product="starch branching enzyme IIa" exon 7641434	omic DNA" i" n:112509"	JOURNAL Plant Physiol. 118 (1), 37-49 (1998) MEDLINE 98404232 PUBMED 9733524 REFERENCE 2 (bases 1 to 1852) AUTHORS Sun,C., Sathish,P., Ahlandsberg,S. and Jansson,C. TITLE Direct Submission JOURNAL Submitted (11-MAY-1998) Stockholm University, Biochemistry, Stockholm S-10691, Sweden FEATURES Location/Qualifiers 1. 1852 1. 1852 1. 1852 1. 1852	REFORMS: KEYWORDS FOR Hordeum vulgare subsp. vulgare ORGANISM Hordeum vulgare subsp. vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. REFERENCE 1 (bases 1 to 1852) AUTHORS Sun,C., Sathish,P., Ahlandsberg,S. and Jansson,C. TITLE The two genes encoding starch-branching enzymes IIa and IIb are differentially expressed in barley	RESULT 3 AF064562 AF064562 AF064562 AF064562 DEFINITION Hordeum vulgare cultivar Bomi starch branching enzyme IIa (sbeIIa) gene, nuclear gene encoding plastid protein, partial cds. ACCESSION AF064562 1 GI: 1851525	Qy 1980 GTTAATGGTCACTATTCACCAACTAGCTTACTGGACTTACAAATTAGCTTACTGAATACT 2039

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           978 AGATACCTGAAGATATCGAGGAGCAAACGGCGGAAGTGAACATGACAGGGGGGACTGCAG
                                                                                                                                                                                                         Unclassified.

1 (bases 1 to 2853)

1 (bases 1, Kroger, C., Lutticke, S. and Lorz, H. Willmitzer, L., Kroger, C., Lutticke, S. and Lorz, H. Nucleotide sequences encoding enzymes that alter concentration and composition in plants

Patent: US 6570066-A 3 27-WAY-2003,

Patent: US 6570066-A 3 27-WAY-2003,
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Best Local Similarity 98.0%;
Matches 246; Conservative
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6-alpha-D-(1,4-alpha-D-glucanotransferase mRNA, complete cds.
U66376
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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6-alpha-D (1,4-alpha-D-glucan)
6-alpha-D (1,4-alpha-D-glucanotransferase")
/product i id="Aal17086.1"
/db xref="GI:1620662"
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/mol_type="mRNA"
/cultivar="T.A. Florida"
/db_xref="taxon:4565"
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  Score 243; DB 8; Length 2853; Pred. No. 4.6e-48; 0; Mismatches 5; Indels
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Best Local Similarity
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1 (bases 1 to 2549)

Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H., Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
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Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum
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/mol_type="mRNA"
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Matches 241; Conserv
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Triticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M.,
Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
starch-branching enzyme IIa from the wheat genome donor Aegilops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae, Triticeae, Triticum.

1 (bases 1 to 2726)
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ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT 1217
                                                                                                                                                                                                                                               AGATACCTGAAGACATCGAGGAGCAAACGGCTGAAGTAAACATGACAGGGGGGGACTGCAG
                                                                                                CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAAACCAGGAG 1157
                                                                                                                                               AAAAACTTGAATCTTCAGAACCGACTCAAGGCATTGTGGAAACAATCACTGATGGTGTAA 319
                                                 CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAAACCAGGAG 379
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="starch branching enzyme IIa variant"
/product="starch branching enzyme IIa variant"
/product="starch branching enzyme IIa variant"
/protein id="MAXZ6822.1"
/db_xref="gi:13147952"
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HLDYRYSEYRRIRAAIDQHEGGLEAFSRYEKIGFTRSAEGITYREWAPGAHSAALVG
DFNNWNPADTWTRDDYGVWEIFLPLNNADGSPAIPHGSRYKIRNDTPSGYVCDSISAWI
KESYQAPGEIPFNGIYYDPFZEEKYVFQHPQPKRPESLRIYSSHIGMSSPEPKINSYA
NFRDEVLPRIKRLGYNAVQIMAIQEHSYYASFGYHVTNWFFAPSSRFGTPEDLKSLIDR
AHELGILVLMDIVHSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHWMWDSRLFNYGSWE
VLRFLLSNARWWLEBYKFDGFRFDGYTSMYTHHGLQHTFTGNYGEYFGFATDYDAVV
YLMLVNDLIHGLHPDAVSIGEDVSGMPTFCIPVDGGVGFDYRLHMAVADKWIELLKQ
SDESNKMGDIVHTLTNRWALEKCVTYALSHDQALVGMTIAFWLMDKOMYDFMALDR
STRRIDRGLALHKMIRLVTMGLGGEGYLNFNGNFFGHPSTSHQYSRKHEEDKV
IIFBRGDLVFVFNFHSNSFSPYRVGGSRPGKYKVALDSDDALFGGFSRLDHDVDYFT
TEHPHDNRPRSFSVYTPSRTAVVYALTE"
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|mol_type="mRNA"
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Pred. No. 4.1e-46;
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polyA_signal

mat_peptide

/gene='

gene="sbe2"

/product="1,4-alpha-glucan branching enzyme
/EC_number="2.4.1.18"

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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 009, CANADA
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Y11282.1 GI:1885343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                             /db_xref="Goredon"
/db_xref="Gor
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151. .2622
                                           ERGDLVFVENFHWSNSFFDYRVGCSRFGKYKVALDSDDALFGGFSRLDHDVDYFTTEH
EHDNRPRSFSVYTFSRTAVVYALTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="1,4-alpha-glucan branching enzyme
/protein id="CAA72154.1"
/db_xref="GOA:P93691"
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/EC_number="2.
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!one="pRN33"
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McCue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D. McCue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D. Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum sestivum cv. Cheyenne): Molecular Characterization, Development in the Cheyense of the American State of the Company of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF286319 2970 bp mRNA linear PLN 14-MAR-2003 Triticum aestivum starch branching enzyme 2 (Sbe2) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUL-2000) United Agricultural Research Service, 94710-1105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum (bread wheat)
Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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2948
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2930. .2935
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                                                                                                                                                                          149. .2620
                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                               'gene="Sbe2"
                                                                                                                                                                                                                                                 tissue_type="endosperm"
                                                                                                                                                                                                                                                                               cultivar="Cheyenne"
db_xref="taxon:4565"
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product="starch branching enzyme
                                                                                                                                                                                                                                                                                                                                                                   organism="Triticum aestivum"
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Pred. No. 4.2e-46;
0; Mismatches 10
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KDSSRAVLSRAASPGKYLVPDGESDDLASPAGPEELQIPEDIEQKIYEIDPTLKDFRSHLD
YRYSEYRRIRAAIDQHEGGLEAPSGRYEELGFTRSAEGITYREMAPGAHSAALVGDFN
NMNPNADTMTRDDYGVMEIFILPNANDGSPAIPHGSRVKIRNDTPSGVVDSISAMIKFS
VQAPGEIPFNGIYYAPPEEEKYVFQHFQPFRPESLRIYESHIGMSSPEPKINSYANFR
DEVLPRIKRLGYNAVQIMAIQEHSYYASFGYHVTNFFTAPSSRAFGTPEDLKSLIDRAHF
LGLLVLMDIVHSSRNNTLDGLNGFDGTDTHYFHGGPRGHHMMNDSRLENYGSMEVLR
FILSNARWHLEEYKFDGFRFDGVTSMMYTHGLQWTFTGNYGEYFGANDVDAVVLM
LVNDLIHGLHPDAVSIGEDVSGMPTFCIPVDGGVGFDYRLMAVADKWIELKKQSDE
SWKMGDIVHTLTMRRWLEKCVTYAESHDQALVGDKTIAFMUDKDMYDFMALDRPSTP
SWKMGDIVHTLMRRWLEKCVTYAESHDQALVGDKTIAFMIDKDMYDFMALDRPSTP
RIDRGIALHKMIRLVTMGLGGEGVLMFYNGNFGHPSWIDFFRAPGOTLLFTGKVLLGNNN
SYDKCRRRFDLGDADFLRYHGMQEFDQAMQHLEEKYGFMTSEHQYVSRKHEEDKVIIF
ERGDLYFVNGNSSFEDYRVGGSRPGKYKVALDSDDALFGGFSRLDHDVDYFTTEH
PHDNRPRSFSVYTPSRTAVVYALTE"
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Matches 240; Conserv
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                                                                                                                                                                  Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 2554)
Sun,C., Sathish,P., Ahlandsberg,S. and Jansson,C.
The two genes encoding starch-branching enzymes IIa and IIb are
differentially expressed in barley
Plant Physiol. 118 (1), 37-49 (1998)
                                                                                        2 (bases 1 to 2554)
Sun,C., Sathish,P., Ahlandsberg,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare cultivar Bomi starch branching enzyme IIa (sbeIIa)
                                                          Submitted (11-MAY-1998) Stockholm Stockholm S-10691, Sweden
                                                                                                                                                      98404232
                                                                                                                                                                                                                                                                                                                                               AF064560.1
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                                             Location/Qualifiers
/mol_type="mRNA"
              organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                               GI:3822019
                                . 2554
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Pred. No. 1e-45;
O; Mismatches
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                                                                             University, Biochemistry,
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211; Conservative
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AY357072.1
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Triticum
(SbeIIa)
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                             Miao, H.M., Han, J.F. and Fleming, J.E. Direct Submission
Submitted (31-JUL-2003) Institute of Biotechnology, Henan Academy of Agricultural Sciences, No.1 Nongye Road, Zhengzhou, Henan Province 450002, China
                                                                                                                                            1 (bases 1 to 3094)
Miao, H.M., Han, J.F. and Fleming, J.E.
Investigation of endosperm-specific promoters
Unpublished
                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                     Triticum aestivum (bread wheat)
Triticum aestivum
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                                                                                                                                (bases 1 to 3094)
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QVVPKPGDGGKIYELIVDFRKHTKDFRSHLDYRGEKRATRAALDQHEGGLEVFSRGYEEKG
FTRSAKGITYREMAPGAHSAALVGDFNNMNPNADTMTRDDYGVMEIFLANDGSPAI
FTRSAKGITYREMAPGAHSAALVGDFNNMNPNADTMTRDDYGVMEIFLANDAGSPAI
PHGSRYKIRMDTPSGVKDSISAMIKFSVQAPGEIFFNGIYYDPPEEEKYVPQHPQPKR
PESILALYESHIGMSSPEPKINGYANFRDEVLIPAIKRLGYNAVQIMLDGHSYYASFGV
HVTNFFAAPSSRFGTPEDLKSLINDFAHELGLLVLNDIVHSHSSNNTLDGLNGFDGTDTH
YFHGGPGHHMMNDSRLFNYGSNEVLRFLLSNARWMLEBYXFDGFREFDGVTSMMYTHH
GLQMTFTGNYGEYFGFATDVDAVVYLMLVNDLIHGLYPDAVSIGEDVSGMPTFCIPVP
DGGVGFDYRLHNAVADKMIELLKQSDESNKVNGDIVHTLEKCVTYABSHDQAL
VGDKTIAFMLMDKDMYDFMALDRFSTFRIDRGIALKMIRLVTMCJGGEGYLNFMGME
FGHPBWIDFRGFQTLFTGKVLFGNNNSYDKCRRRFDLGDADFLRYRGMQEFDQAMQH
LEEKYGFMTSSHQYVSRKHEEDKVIIFERGDLVFVFNHRMNSKKDYRVGCSKPGKYK
LEEKYGFMTSSHQYVSRKHEEDKVIIFERGDLVFVFNHRMNSKTDYRVGCSKPGKYK
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/product="starch branching enzyme IIa"
/protein_id="AAC69753.1"
/db_xref="GI:3822020"
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/db_xref="taxon:112509"
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/EC_number="2.
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               Location/Qualifiers
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   Fu, G., Wang, S.Y.,
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3066 CTGGCTGACTCAATCACTACGCGGGGATG 3094
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Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu,S., Tang,Y.,
Wang,Q., Zhang,L., Lu,Y., Mu,J., Lu,Y., Zhang,L.S., Yu,Z., Fan,D.,
Liu,X., Lu,T., Li,C., Wu,Y., Sun,T., Lei,H., Li,T., Hu,H., Guan,J.,
Wu,M., Zhang,R., Zhou,B., Chen,Z., Chen,L., Jin,Z., Wang,R.,
Yin,H., Cai,Z., Ren,S., Lv,G., Gu,W., Zhu,G., Tu,Y., Jia,J.,
Zhang,Y., Chen,J., Kang,H., Chen,X., Shao,C., Sun,Y., Hu,Q.,
Zhang,X., Zhang,W., Wang,L., Ding,C., Sheng,H., Gu,J., Chen,S.,
Ni,L., Zhu,F., Chen,W., Lan,L., Lai,Y., Cheng,Z., Gu,M., Jiang,J.,
Li,J., Thong,G., Xue,Y. and Han,B.
Sequence and analysis of rice chromosome 4
Nature 420 (6913), 316-320 (2002)
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HTG; HTGS PHASE2.
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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/cultivar="Yumai-18"
/db_xref="taxon:4565"
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<1. .>3094
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/protein_id="AAQ64002.1"
/db_xref="GI:34329815"
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/EC_number="2.4.1.81"
/note="glucosyltransferase"
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/gene="SbeIIa"
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2684. .2689
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100.0%; Pr
Ren, S.X.,
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Lv, G., Lin, W.,
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Gu, W.Q.,
     Zhu, G.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/cddy/tRNAscan-SE/), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/da) and the EST database at NCGR.
* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bhandnogr ac.cn
Cryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone: OSZNBA0042115.
On Jul 9, 2003 this sequence version replaced gi:21912624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-MAY-2002) Han Bin, National Center for Gene Research, Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a PHASE2 sequence. Gaps are shown by 200n. Genes were identified by a combination of several methods: Gene prediction programs including Figensesh (http://www.softberry.com/), genscan (http://ccr-081.mit.edu/GENSCAN.html), GeneMarkHMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Hong, G.F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: phrap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by the finished sequence as soon as it is available and the accession number will be preserved.

1 9353: contig of 9353 bp in length 9354 47134: contig of 37581 bp in length 47135 4734: gap of 200 bp 51471 51670: gap of 200 bp 51471 62557: contig of 4136 bp in length 62558 62757: gap of 200 bp 62758 62758 9833: contig of 19878 bp in length 62758 62757: gap of 200 bp 102631 102830: gap of 200 bp 102831 102830: gap of 200 bp 102830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/
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142542: gap of
159683: contig
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of 17141 bp
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                                                              GQRSASFHGRGTEPWHQLARQRPKTQPDLLAGVRGRATAASFGPAAAAGGGEQLEPEA
AGRRTPSKVLVSVAVQRSLWPLHVMASAAWSVADLVAAAVALYVKEGRRPPLPSADPS
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GSRYAVQRSGNILMAFNNKEASLAVPLFSPVIVPMAQSFGPIFSQLTSYPTLRFGVKS
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LAHLGGNHSAAGNGDDDEYESTQQHRIKCAGFFGGLGAAPPTSSSYWLSAADGATAA
APSARTHGARSHRSWAWALASPMRALRPTSSSSKSIVAAPHNRGGVSGNGGMAWAAV
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12175. .12244,12325. .12611))
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EKLQFIIRVSIVRDDSSIAFKGVLKGDLYLVDFDVDRVNPEACLIAKSSMCWLMHRRL
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LHWDLFGFVAYISIGGNKYGFVIVDDFSCFTWVFLHKGKGAQDLYDFKRFTLIEAARAM
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IGDIRPVETQDDQEDRDQPPSSTSNSPTSVVSAEPEVPGPIDRNLRTSPGPEVPGSTV
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E14724.1 GI:570940
E14724.1 JP 1998004970-A/2.
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacese; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacese; Enrharcoideae; Oryzeae; Oryza.

1 (bases 1 to 2364)
Baba, T., Kawasaki, T. and Ichikawa, N.
Baba, T., Kawasaki, T. and Ichikawa, N.
BEW RICE GENE FOR STARCH-BRANCHING ENZYME
Patent: JP 1998004970-A 2 13-JAN-1998;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LTD OS Oryza sativa (rice)
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PD 13-JAN-1998

PD 13-JAN-1998

PF 24-JUN-1996 JP 1996162983

PF 24-JUN-1996 JP 1996162983

PI BABA TADASHI KAMASAKI TSUTONU, ICHIKAWA NORIO PC C12N15/09, A01H5/00, C07H21/04, C12N5/10, C12N9/10, C12N9/10, C12N15/09, PC C12R1:91), (C12N1-91), (C12N9/10, C12N1:19);

PC (C12N5/10, C12R1:91), (C12N9/10, C12R1:19);

PC (C12N5/10, C12N1:19);

PC (C1
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

DE 1 (bases 1 to 3015)

RS Baba, T., Kawasaki, T. and Ichikawa, N.

NEW RICE GENE FOR STARCH-BRANCHING ENZYME
NEW RICE GENE FOR STARCH-BRANCHING ENZYME
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LID
OS Oryza sativa (rice)
PN JP 1998004970-A/1

PD 13-JAN-1998
PF 24-JUN-1998 JP 1996162983
PF 24-JUN-1996 JP 1996162983
PF 24-JUN-1996 JP 196162983
PF 24-JUN-1996 JP 196162983
PF 24-JUN-1996 JP 196162983
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PF 24-JUN-1996 JP 1976162983
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Rice mRNA for branching 6
E14723
E14723.1 GI:5709406
JP 1998004970-A/1.
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Oryza sativa
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:4530"
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/culivar='Nihonbare'
/clone_lib='Rise Immature
/ library'
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Pred. No. 7e-22;
0; Mismatches 52;
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/clone='pRB41'
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enzyme-4,complete cds.
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Oryza sativa
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Oryza sativa mRNA for starch
AB023498
                                                                                                    2 (bases 1 to 3015)
Mizuno,K. and Baba,T.
Mizuno,K. and Baba,T.
Submission
Submitted (09-FEB-1999) Kouichi Mizuno,
Institute of Agricultural and Forest Eng
Tsukuba, Ibaraki 305-8572, Japan
                                                                                                                                                                                                         Mizumo,K., Tachibana,M., Kobayashi,E., Kawasaki,T., Funane,K., Kobayashi,M. and Baba,T.
Kobayashi,M. and Baba,T.
Molecular cloning and expression analysis of a novel member of starch branching enzyme isoform in developing rice seeds
                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                  starch branching enzyme
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                                                                           Fax:81-298-55-2203)
                                                                                        Tsukuba, Ibaraki 305-8572, Japan
(E-mail:koumno@sakura.cc.tsukuba.ac.jp,
                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                        starch branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGACATTGAGGAAAATGTGACTGAGGGTGTGATCAAAGATGCTGATGAACCAACTGTGGA 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGCTGGAAGGATTTCGGAACCATCTTGACTACCGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATAAAACCACGAGTTATCCCACCACCAGGAGATGGGCAGAAGATATACCAAATTGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
                                                             Location/Qualifiers
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/clone='pRB41'
129. .2654
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/cultivar='Nihonbare'
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Pred. No. 7.5e-22;
0; Mismatches 52;
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| library'
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branching 6
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                                                                                                                       Engineering;
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                                                                                                                        University of Tsukuba,
gineering; 1-1-1 Tennoudai,
                                                                                             Tel:81-298-53-4656
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The invention relates to a novel enzyme of starch biosynthetic pathway in a cereal plant, where the enzyme is selected from starch branching enzyme (SBE) I , SBE II, starch soluble synthase (SSS) I, and debranching enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of

Claim 8; Page 75-81; 171pp; English.

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ALIGNMENTS

AAX34650 standard; DNA; 11473

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05-JUL-1999
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20-MAR-1998;
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98AU-00002509.
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Oy 601 TTGCAGGCGCCGTCCTGAGCGCGCGCCCCTTCTCCAGAAGGTCCTGGTGCCTGAGGCACCTGTCCTGAGGAAGGTCCTGGTGCCTGAGGCAAGGTCCTGAGGAAGGTCCTGATGCAGGCGTCCTTGAGGCAAGGTCCTGAGGAATTACAGGTACACACCTGAGGAGGCCCTGAGGAATTACAGGTACACACAC	361 GCTGTTCCCCAATTGATCTCCATGAGTGAGAGAGAGATAGCTGGATTAGG	QY 121 CTGGCTGACTCAATCACTACGCGGATTGGCGACGTTCGCGGCTGCCGACTCTCG	cc rice or maize. The methods and products can be used for targeting cc expression specifically to the endosperm of the seeds of cereal plants cc such as wheat or barley. They can be used for the expression of e.g. cc antisense sequences of granule-bound synthase (GBSS), SBE II, low mol. cc glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be used for modifying the characteristics of starch produced by a plant. The cc present sequence represents the SBE II gene sequence. (Updated on 17-CCT-CC 2003 to standardise OS field) XX Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other; Query Match Best Local Similarity 99.1%; Score 2127; DB 2; Length 11473; Best Local Similarity 99.5%; Pred. No. 0; Indels 10; Gaps 1 OY 1058 CGCCAGCTTCCACCCCCCGCCGCACACGTTGCTCCCCCTTCTCATCGCTTCTCAATTAATA 60 1058 CGCCAGCTTCCACCCCCGCCGCACACGTTGCTCCCCCTTCTCATCGCTTCTCAATTAATA 111. OY 61 TCTCCATCACTCGGGTTCCGCGCTGCATTTCGGCCGGCGGGTTGAGTGAG
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TIGATTIGAAGCATTITICICGTGTTATGAAAAGCTTGGATTTACCGCAGGTAAATTTA AAGCTTTATTATTATTATGAAAGCGCTCCACTAGTCTAATTGCATATCTTATTAAGAAAATTTA AAGCTTTATTATTATGAAAGCGCCTCCACTAGTCTAATTGCATATCTTATAAGAAAATTTA AAGCTTTATTATTATGAAACGCCTCCACTAGTCTAATTGCATATCTTATAAGAAAATTTA TAATTCCTGTTTTCCCCTCTCTTTTTTCCAGTGCTGAAGGTATCGTCTAATTGCATATCT TAATTCCTGTTTTCCCCTCTTTTTTCCAGTGCTGAAGGTATCGTCTAATTGCATATCT TATAAGAAAATTTATATTCCTGTTTTTCCCCTATTTTCCAGTGCTGAAGGTATCACTTACC TATAAGAAAATTTATATTCCTGTTTTTCCCCTATTTTCCAGTGCTGAAGGTATCACTTACC GAGAATGGGCTCCCTGAGGTATCCTCTATTTCCAGTTCTTAAGGTATCACTTACC GAGAATGGGGCTCCCTGAGGTATCTTTTCCCCTATTTTAAGTTCCTTAAGGAGACACCCTTC [ANAGAGTGGCANACTGATGAAAATGTGGTGGATGGGTTATAGATTTACTTTGCTAATTC CTCTACCAAATTCCTAGGGGGGAAATCTACCAGGTTGGGAAACTTAGTTTCTTATCTTTGT CTCTACCAAATTCCTAGGGGGGAAATCTACCAGTTGGGAAACTTAGTTTCTTATCTTTGT CTCTACCAAATTCCTAGGGGGGAAACTAACTAACTTAGTTTCTTATCTTTGT GGCCTTTTTGTTTTG	TCGGAGCCATCTTGACCAGATAGCCTACCAATGCCTACCGATCCTTCGCTACTACTACTACGATTAAGGCCATCTTCACCAATGCCTACCCGCTGCTTTCCACTACTAGAGACAAATGTTGGGGAACAACAAAGACAAAAGACTAAGGGCTACGCTACGCTACTAGGGTIGIIIIIIIIII	

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Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other; Query Match Best Local Similarity 99.9%; Score 2124; DB 5; Length 11475; Best Local Similarity 99.9%; Pred. No. 0; Matches 2146; Conservative 0; Mismatches 0; Indels 2; Gaps 2; Matches 2146; Conservative 0; Mismatches 0; Indels 2; Gaps 2; Y 1 CGCCAGCTTCCACCCCGCCGCACACGTTGCTCCCCTTCTCATTCGTTCTCAATTAATA 60	Example 1; Fig 2; 103pp; English. The present sequence encodes a wheat starch branching enzyme of Aegilops tauschii, designated F2. A. tauschii is likely to be the ancestral D genome donor of wheat. Probes isolated from the present sequence were used to identify type II starch branching enzymes (SBEs) in wheat, especially BEIIb. The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant	Morell M, Rahman S; WPI; 2001-570635/64. Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat and barley.	21-FEB-2001; 2001WO-AU000175. 21-FEB-2000; 2000AU-00005742. (CSIR) COMMONWEALTH SCI & IND RES ORG. (GOOD-) GOODMAN FIELDER LTD. (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	starch biosynthetic pathway; amylopectin; P2; amylose; ss. Aegilops tauschii. WO200162934-A1. 30-AUG-2001.	8 standard; cDNA; 11475 BP. 8; 2001 (first entry) ide sequence of a starch branching enzyme design	2978 GAGAATGGGCTCCCTGGAGCGCATGTTATGTTCTTTAAGTTCCTTAACGAGACACCTTC 3037 1971 CAATTTATTGTTAATGGTCACTATTCACCAACTAGCTTACTGGACTTACAAATTAGCTTA 2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CSIR ) COMMONWEALTH SCI & IND RES ORG
(GOOD-) GOODMAN FIELDER LTD.
(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
                                                                                                                                  AAH78353 standard; DNA; 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH78351-54 represent intron 5 fragments from wheat.
                                                    Nucleotide
                                                                                26-NOV-2001
                                                                                                           AAH78353;
                                                                                                                                                                                                                                                                                                                                                                                        1901
                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  starch branch
biosynthetic
             starch branching enzyme; BEIIb; SBE; transgenic plant; biosynthetic pathway; amylopectin; amylose; ss.
                                                                                                                                                                                                                                                                                                                                                                μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ďв
                                                                                                                                                                                                                                                                                                                                   AGACACCTTCCAATTTATTGTTAATGGTCACTATTCACCAACTAGCTTACTGGACTTACA
                                                                                                                                                                                                                                                                               AATTAGCTTACTGAATACTGACCAGTTACTATAAATTTATGATCTGGCTTTTGCACCCTG
                                                                                                                                                                                                                                                                                                        AGACACCTTCCAATTTATTGTTAATGGTCACTATTCACCAACTAGCTTACTGGACTTACA
                                                                                                                                                                                                                                                                                                                                                                                        ATCACTTACCGAGAATGGGCTCCCTGGAGCGCATGTTATGTTCTTTTAAGTTCCTTAACG 1960
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                                                                                                                                                                                                                                                                                                                                                             ATCACTTACCGAGAATGGGCT-CCTGGAGCGCATGTATGTCTTTTAAGTCTT-----AAC
                                                                                                                                                                                                                                                        AATTAGCTTACTGAATACTGACCAGTTACTATAAATTTATGATCTGGCTTTTGCACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rahman S;
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-AU000175
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thetic pathway; amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0f
                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%;
                                                    of intron 5
                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron 5 fragment from
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 177.6; I
Pred. No. 1.1e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amylopectin; amylose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BEIIb;
                                                      fragment from B genome of wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SBE; transgenic plant;
in; amylose; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     1.1e-39;
thes 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome of wheat
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification
                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                        2020
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RESULT 6
AAH7832
ID AAH7
XX AAH7
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XX Whea
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XX Trit
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PN WO20
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PN SCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim
Matches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH78351-54 represent intron 5 fragments from wheat. The specification describes a wheat starch branching enzyme, designated BEIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat and barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CSIR )
(GOOD-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2000; 2000AU-00005742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2001; 2001WO-AU000175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 217 BP; 63 A; 47 C;
                                                                                                                             Wheat; starch branching enzyme; BEIIb; starch biosynthetic pathway; amylopecti
                                                                                                                                                                     Nucleotide
                                                                                                                                                                                                                                                   AAH78352 standard; DNA; 228
                           21-FEB-2001;
                                                                                                                                                                                                26-NOV-2001
                                                                                                                                                                                                                          AAH78352;
                                                                             WO200162934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1956 TAACGAGACACCTTCCAATTTATTGTTAATGGTCACTATTCACCAACTAGCTTACTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-570635/64.
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                                                                                                                                                                                                                                                                                                                   161
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GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC PTY LTD
                                                                                                      ďs
                                                                                                                                                                                                                                                                                                                   TCCTGTTACAGTCTGCAGCATTAGTAGGTGACTTCAACAATTGGAATCCAAATGCAG
                                                                                                                                                                                                                                                                                                                                        CCCTGTTACAGTCTGCAGCATTAGTAGGTGACTTCAACAATTGGAATCCAAATGCAG 2132
                                                                                                                                                                                                                                                                                                                                                                     TTACAAAATAGCTTACTGAATACTGACCAGTTACTCTAAATTTATGATCTGGCTTTTGGA
                                                                                                                                                                                                                                                                                                                                                                                               TTACAAATTAGCTTACTGAATACTGACCAGTTACTATAAATTTATGATCTGGCTTTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                          TTAACAGACACCTTCTAATTTATTGTTAATGGTCACTATTCACCAACTAGCTTACTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rahman S;
                                                                                                                                                                      sequence of intron 5 fragment from A genome of wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                            2001WO-AU000175
                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.6%;
                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                    BP
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Pred, No. 6.7e-36;
0; Mismatches 8
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                                                                                                                                amylopectin; amylose; ss
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                                                                                                                                               SBE; transgenic
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                                          Length
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2000AU-00005742

(CSIR) (GOOD-)

COMMONWEALTH SCI & IND RES GOODMAN FIELDER LTD. GRP LIMAGRAIN PACIFIC PTY

DIY YIG

ORG

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RESULT 7
AAVU5639
ID AAVU
XX AAVU
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DT 01-W
XX Rice
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Best Local S
Matches 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH78351-54 represent intron 5 fragments from wheat. The specification describes a wheat starch branching enzyme, designated BSIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-570635/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                Rice type IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
01-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV05639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV05639
                                                                                                                                                 mat_peptide
                                                                                                                                                                                               sig_peptide
                                                     JP10004970-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208;
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                                                                                                                                                                                                                                                                                                                                                                     type IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAATTAGCTTACTGAATACTGACCAGTTACTATAAATTTATGATCTGGCTTTTGCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACACCTTCCAATTTATTGTTAATGGT--CACTATTCACCAACTAGCTTACTGGACTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rahman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     starch branching enzyme cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                            starch
                                                                                                                                                                     /*tag= a
129. .287
/*tag= b
                                                                                                                                                      288.
                                                                                                                                                                                                                                               Location/Qualifiers
129. .2654
                                                                                                   'product=
                                                                                                                               *tag=
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88.9%;
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                                                                                                                                                   .2651
                                                                                                                                                                                                                                                                                                                                                                       branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to mRNA;
                                                                                                   "type_IV_starch_branching_enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 159.2; I
Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       enzyme; amylopectin synthesis;
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ches 18;
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PET COLOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MITS-)
                                                                                                                                                                                                                                                                    LT 8
1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes the rice type IV starch branching enzyme, which has the ability to synthesise amylopectin. The quality of starch improved by the use of the protein. (Updated on 25-MAR-2003 to correct field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice starch branching quality starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-133625/13.
P-PSDB; AAW41763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1996;
                   Chang H,
Katagiri
                                                                                                                                                 Oryza sativa
                                                                                                                                                                  Plant; bacterial gene; ds.
                                                                                                                                                                                             Rice gene, SEQ ID 4612
                                                                                                                                                                                                                  20-NOV-2003
                                                                                                                                                                                                                                     ADA71289;
                                                                                                                                                                                                                                                        ADA71289
                                                                                       22-JUN-2001; 2001WO-IB001105
                                                                                                           03-JAN-2003
                                                                                                                             WC2003000898-A1
                                                                   22-JUN-2001; 2001WO-IB001105
                                                (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                              1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                   Chen W, F, Quan
                                                                                                                                                                                                                                                                                                                                                                                                     GGGCATTGTGGAAACAATCACTGATGGTGTAACCAAAGGAAGTTAAGGAACTAGTCGTGGG 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3015 BP; 796 A; 606 C; 819 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 5-8;
                                                                                                                                                                                                                                                                                                                            AACACTGAAAGATTTTCGGAGCCATCTTGACTACCGGTA 1224
                                                                                                                                                                                                                                                                                                                                                                  ggagaaaaccgcgagttgtcccaaaaaccaggagatgggcagaaaatatacgagattgaccc
                                                                                                                                                                                                                                                                                                                                                                                    AGACATTGAGGAAAATGTGACTGAGGGTGTGATCAAAGATGCTGATGAACCAACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                            GGCAGAAGCAAGCATAAAGGTTGTGGCTGAAGACAAACTTGAATCTTCAGAAGTGATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGGAAGTGAACATGACAGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCA
                                                                                                                                                                                                                                                                                                                                              GGATAAACCACGAGTTATCCCACCACCAGGAGATGGGCAGAAGATATACCAAATTGACCC
                                                                                                                                                                                                                                                          standard; DNA;
                                                                                                                                                                                                                                                                                                        AATGCTGGAAGGATTTCGGAACCATCTTGACTACCGATA
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                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                             infection; fungal infection; viral infection; rice;
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                    Cooper |
S, Tao
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Pred. No. 3.4e-27;
                                                                                                                                                                                                                                                           BP.
                    Glazebrook J, Goff\SA, whitham S, Xie Z, Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                   AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthesises amylopectin
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WPI; 2003-175290/17

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method (MI) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
22-JUN-2001;
26-SEP-2001;
20-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2655 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; SEQ ID NO 4612; 899pp; English.
                                                                                                                                                                                                      carbohydrate degradation; carbohydrate; plant grain; grain filling;
tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
wheat; rice; protein; oil; starch; fibre; moisture content; cereal g
                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                  plant
                                                                                                                                                                                                                                                                                 Rice DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       illustrate the invention.
                                                                                                                                                        Oryza
                                                                                                                                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                              ADC08218;
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                                                            21-JUN-2002;
                                                                                                                           WO2003000905-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1218
                                                                                                                                                        sativa
                                                                                                                                                                                    ds; plant.
                                                                                                                                                                                                                                                   biotechnology; carbohydrate synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCEGTAAT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAAAGGAGTTAAGGAACTAGTCGTGGGGGGAGAAACCGAGTTGTCCCAAAACCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                             standard; DNA;
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 2001US-0300112P.
2001US-0325277P.
2001US-0342327P.
                                                               2002WO-IB002450
                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                               Seq ID523 related to grain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                        carbohydrate metabolism;
t grain; grain filling; c
                                                                                                                                                                                                                                                                                    filling.
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Best Local Similarity
Matches 164; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New plant genes encoding polypeptides having an activity involved in associated with the synthesis, metabolism or degradation of carbohydin the plant grain useful in generating plants having improved
                                            Wheat;
starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                            Nucleotide
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                                            starch brancl
biosynthetic
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                                                                                                                                                                                                                                                                                            ACCG 1221
                                                                                                                                                                                                                                                                                                                                                                                                                CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGGGAGTTGTCCCCAAAACCAGGAG
                                                                                                                                                                                     standard; cDNA; 2968
                                                                                                                                                                                                                                                                                                                        ATGGGCAGAAGATATACCAAATTGACCCAATGCTGGAAGGATTTCGGAACCATCTTGACT
                                                                                                                                                                                                                                                                                                                                                   ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT
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                                                                                                                                                                                                                                                             ACCG 530
                                                                                          sequence of wheat starch branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.4%;
ilarity 67.2%;
Conservative
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Katagiri 1
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                                                           enzyme;
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Kreps J,
                                              ne; BEIIb; SB
amylopectin;
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, Provart
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.2e-21;
                                                 amylose) ss.
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Ricke D;
                                                                                               (BEIIb)
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a wheat starch branching enzyme, designated BEIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or bearley and for altering their nutritional content by modulating the starch blosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 9; 103pp; English.
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                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                  Wheat; starch branching enzyme; starch synthesis; wdk2c.pk009.j17; antibody; gene mapping; expresse
                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2002
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                                                                                                                                                               Triticum aestivum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGTGAACATGACAGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2968 BP; 784 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; cDNA; 3039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGCCTA 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATTACGCATTCTGCCACCACCGGAAATGGACAGCAAATATACGAGATTGACCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACCGCGAGTTGTCCCAAAACCAGGAGATGGGCAGAAAATATACGAGATTGACCCAACA 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGAAGAAATTGATGCTGAAGACACGAGCAGAATGGACAAAGAATCATCTACGAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGTGGAAACAATCACTGATGGTGTAACCAAAGGAGTTAAGGAACTAGTCGTGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAACAAGCCTACAGGATGGAGGTGAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rahman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%;
nilarity 61.3%;
Conservative
                                                                                                                                                                                                                                                                                                                branching enzyme IIb cDNA from
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
  /*tag= a
/product=
/partial
                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  626 C;
                                   "Starch branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 84.4; DI
Pred. No. 1.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>۾</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; DB 5;
1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     756 T; 0
                                                                                                                                                                                                                                        expressed
                                enzyme IIb"
                                                                                                                                                                                                                                                                                                                   clone wdk2c_pk009.j17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٦;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                          transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1069
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CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGCCTA

AAATTACGCATTCTGCCACCACCGGGAAATGGACAGCAAATATACGAGATTGACCCAACG даассеселеттетсссалалссаеватеееслевалататаселеаттелессанся 1189 AGTGAAGAATTGATGCTGAAGACACGAGCAGAATGGACAAAGAATCATCTACGAGGGAG

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This invention relates to the cDNA and protein sequences of a novel wheat companies to the cDNA and protein sequences of a novel wheat starch branching enzyme IIb enzyme. Starch branching enzymes are constant synthesis pathway. The nucleotide sequence in amylopectin in the constitution by the formation of alpha 1-6 linkages in amylopectin in the constitution synthesis pathway. The nucleotide sequence of the invention is constituted by the starch branching at transgenic plant expressing the starch branching construction is constituted by the construction of the protein is constituted by the constitution of the protein is constituted by the construction of the protein is constituted by the constitution of expression of a starch branching enzyme IIb protein or enzyme construction is useful as markers for traits linked to those genes. This construction is useful in plant breeding in order to develop lines with consider and penson encoding homologous proteins from the same or other plant considers. They are also useful as DNA hybridisation probes or as construction fragment length polymorphism markers. Nucleic acid probes construction fragment length polymorphism markers. Nucleic acid probes constructed from the cDNA sequence may also be used for physical mapping or for fluorescence in situ hybridisation (FISH) mapping. The present construction constructs the wheat starch branching enzyme IIb cDNA from clone constructs.
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                                                                                                            Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated polypeptide having starch IIb enzyme activity, use preparing antibodies to the proteins which are used to detect the polypeptides in situ in cells or in vitro in cell extracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2000; 2000US-0186098P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-2001; 2001US-00792127.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002002713-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 17-18; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALLE/)
(BECK/)
(BUTL/)
                                                                                                                                                                                  Sequence 3039 BP; 836 A; 624 C; 783 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-178959/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALLEN S M.
BECKLES D M.
BUTLER K H.
PEARLSTEIN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLEN
                                                                     GAAGTGAACATGACAGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGC 1069
ATTGTGGAAACAATCACTGATGGTGTAACCAAAGGACTTAAGGAACTAGTCGTGGGGGAG 1129
                                      GAAACAAGCCTACAGGATGGAGGTGAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beckles DM,
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "No start codon shown. The sequence from nucleotides 481-3039 is specifically claimed in of the specification and is shown as Seq ID. 1
                                                                                                                             3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Butler KH,
                                                                                                              0;
                                                                                                                Score 84.4; DB 6;
Pred. No. 1.3e-12;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pearlstein
                                                                                                                                                                                        796 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽,
                                                                                                                                                   Length 3039;
                                                                                                                    Indels
                                                                                                                                                                                           0 Other;
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ις (2)

CTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTA 593

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RESULT 12
AAH78341
ID AAH78
XX AAH78
AC AAH78
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Best Local Similarity
Matches 132; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a partial genomic sequence of a wheat starch branching enzyme of Aegilops tauschii, designated F2. A. tauschii is likely to be the ancestral D genome donor of wheat. Probes isolated F2 were used to identify type II starch branching enzymes (SBEs) in wheat, especially BEIIb. The BEIIb nucleic acids may be used to genetically transform cereal plants such as who are been and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CSIR )
(GOOD-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wheat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3962 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morell
1336
                                                                                                                                                                                                                                  1216
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GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC PTY 1
                                                                                                                                                                    APACCGCGAGTTGTCCCAAAACCAGGAGATGGGCAGAAAATATATACGAGATTGACCCAACA 1189
                                                                                                                                                                                                                                                                                                                                                           GAAACAAGCCTACAGGATGGAGGTGAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTT 1215
                                                                                                                                                                                                                                                                                                                                                                                                               CTCCGAGACTTTAAGTACCATCTTGAGTATCGGTA
                                                    CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTA 1224
                                                                                                                                                                                                                                     AGTGAAGAATTGATGCTGAAGACACGAGCAGAATGGACAAAGAATCATCTACGAGGGAG
                                                                                                                                                                                                                                                                                             <u> АТТСТССАВАСААТСАСТСАТССТСТВАССАВАССТВАССВАСТВСТССТССССССАВ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%;
nilarity 61.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1091 A; 778 C; 809 G; 1284 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82.2; DB 5;
Pred. No. 6.2e-12;
0; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
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RESULT

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RESULT 14
AAQ73750
ID AAQ73
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AC AAQ73
XX

standard; cDNA to mRNA;

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AAQ73750. AAQ73750

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Best Local S
Matches 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH78343 standard;
                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding wheat starch branching enzyme IIb, useful altering the amylose and amylopectin content of cereal plants, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Partial genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2001
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                                                                                                                                                                                                                                           Sequence 8381 BP; 2134 A; 1788 C; 1829 G;
                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 95-98; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CSIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000; 2000AU-00005742.
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                      1190
                                                                                                                                                                                             132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                starch branching enzyme; BEIIb; SBE; transgenic plant; biosynthetic pathway; amylopectin; amylose; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMONWEALTH SCI & IND GOODMAN FIELDER LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRP LIMAGRAIN PACIFIC PTY LTD
                                                                                                                                                                                                         Similarity
                                                                                                                                              GAAACAAGCCTACAGGATGGAGGTGAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTT
                                                                                                                     <u> АТТСТССАВАНСАВТСАСТСАТССТВАВССВАВСЕТАВСЕВАВСТВСТССТСССССВЕ</u>
                                                                                                                                                                    CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTA
                                               AAATTACGCATTCTGCCACCACCGGGAAATGGACAGCAAATATACGAGATTGACCCAACG
                                                                     AAACCGCGAGTTGTCCCAAAACCAGGAGATGGGCAGAAAATATACGAGATTGACCCAACA
                                                                                               AGTGAAGAATTGATGCTGAAGACACGAGCAGATGGACAAAGAATCATCTACGAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rahman
                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry
                                                                                                                                                                                                         3.8%;
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                                                                                                                                                                                             °.
                                                                                                                                                                                             Score 82.2; DI
Pred. No. 9.5e
0; Mismatches
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                                                                                                                                                                                                            DB 5;
5e-12;
                                                                                                                                                                                                                                             2608 T; 0 U; 22 Other;
                         1224
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Rice starch branching enzyme

05-JUL-1995

(first entry)

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RESULT 15
ADC07807
ID ADC07
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AC ADC07
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5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza
                                                                                                                                                                                                                                                                                                                                                             The rice starch branching enzyme is encoded by the cDNA sequence AAQ73750. The starch content of rice grains can be increased by increasing the expression of branching enzyme in rice plants
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 9-12; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                              New gene of branching enzyme of rice starch - useful for increasing starch yield of grain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-337418/42.
P-PSDB; AAR60811.
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                                                                                                                                                                                                                                                      GGAGGTTGGAGCTGAAGTTGAGATTGAGTCATCTGGAGCAAGTGACGTTGAAGGCGTGAA 495
                                                                                                                                                                                                                                                                           GAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGTAAC 1098
                                                                  standard; DNA; 2307
                                                                                                                                           CCGGTAATGCCTA 1231
                                                                                                                                                                                                            GAGAGTGGTTGAAGAATTAGCTGCTGAGCAGAAACCACGAGTTGTCCCACCAACAGGAGA
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                                                                                                                      TCGATATAGCCTA 628
                                                                                                                                                                 TGGGCAAAAATATTCCAGATGGACTCTATGCTTAATGGCTATAAGTACCATCTTGAATA
                      (first entry)
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Pred. No. 3.2e
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  grain filling
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Matches 95
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                                                                                                                                                                                                        This invention, in the area of plant biotechnology, relates to novel polymicleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
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Glazebrook J, Katagiri I
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26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
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                                                                                                                                                                           Sequence 2307 BP; 608 A; 465
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                                       364
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                                                                                                                         Similarity
 GGAAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCCGCAG 1721
                                                            AACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGA-CCAACATGAAGGTGGATT 1676
                                       ACCGGATACAGTGAATACAAGAGAATGCGTGCAGCTATTGACCCAACATGAAGGTGGCTT
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Search completed: April 10, 2004, 04:00:00 Job time : 846.046 secs

В

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GGATGCATTTTCTCGTGGTTACGAAAAGCTTGGATTCACCCGCAG

468

Rice DNA sequence Seq ID73

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is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/pCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-609-040-3
US-09-731-166-9
US-08-237-463-14
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LENGTH: 2853
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Best Local
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ALIGNMENTS

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Sequence 3, Application US/09609040

Patent No. 6570066

GENERAL INFORMATION:
APPLICANT: Willmitzer, et al.
TITLE OF INVENTION: MUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATI
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS
FILE REFERENCE: 514413-3515.1

CURRENT APPLICATION NUMBER: US/09/609,040

CURRENT FILING DATE: 190-06-30

PRIOR FILING DATE: 199-02-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: CDS
LOCATION: (313)..(2499)
OTHER INFORMATION: BRANCHING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                     h 11.3%;
Similarity 98.0%;
46; Conservative
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                                                                                                                                                                   CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAACCAGGAG
                                                                       ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT
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ACCGGTAATGC 1228
                                          ATGGGCAGAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT
                                                                                                                             CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAACCAGGAG
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GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
APPLICANT: Singletary, G
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Patent No. 6639126
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SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: SBEIIA
OTHER INFORMATION: Genbank Accession No. 6639126 U65948
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LOCATION: (2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1800 Dia:
CITY: Alexandria
                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1127
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            US/07/935,313
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 7218 base pairs
TYPE: nucleic acid
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                        579 CTATTGTAGTCATCCTTGCATTTTGCAGGCGCCGTCCTGAGCCG
                                                                        519 TATTITCTCATTCTTTCTTCCTGTTCTTGCTGTAACTGCAAGTTGTGGCGTTTTTTCA 578
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                                                                                                                             GTGTCACCCAGGCCCTGGTGTTACCACGGCTTTGATCATTCCTCGTTTCATTCTGATATA 518
                                                                                                                                                      TCGGAGCGGAGGGGGGGGGACTTGCCGTCGCTCCTCAGGAAGAAGGACTCCTCT 278
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139.
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                                                                                                                                                                                                                                                                                                                                                              3.2%; Score 68.8; DB 1; ilarity 4.7%; Pred. No. 2.7e-09; Conservative 234; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-09-731-166-11
US-09-731-166-11
Sequence 11, Application US/09731166
PATEUR NO. 6639126
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singlatary, George W.
TITLE OF INVENTION: Production of Modified Polysaccarides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2720
TYPE: DNA
ORGANISM: Zea mays
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Query Match
Best Local Similarity
Matches 74; Conserv
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APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE, DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                    TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
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OTHER INFORMATION: Genbank Accession No.
NAME/KEY: CDS
LOCATION: (101)...(2500)
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
                                                                           STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
-257-894-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 2.9%;
Local Similarity 76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/257,894 FILING DATE:
                                                                                                                              LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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2.7%;
ilarity 74.0%;
Conservative
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Pred. No. 1.9e-07;
0; Mismatches 24
  Score 58.4; DB 4;
Pred. No. 1.4e-06;
D; Mismatches 26;
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                                      Length 2087;
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RESULT 6
US-09-257-894-8/c
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; MOLECULE TYPE:
US-09-257-894-8
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В
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; Patent No.
; GENERAL IN
                                                                                                                                                                                                                                                                       TELEFAX: 302-773-010*
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2165 base pairs
TYPE: nucleic acid
                                                                                                                                            Matches
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09,
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/09:
APPLICATION NUMBER: 10, 1990
FILING DATE: JUNE 10, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Broglie,
APPLICANT: Klein, Th
APPLICANT: Hubbard,
APPLICANT: Lightner,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IF Compatible
COMPUTER: COMPATIBLE
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          NAME: Majarian, William R.
REGISTRATION NUWBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Wilmington STATE: Delaware
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                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                     1675 GGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAG
                                                                                                      1622 GATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGGAAG
                                   1682 CATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
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5. 6376749
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CCTTCTCCCGTAGTTATGAGAAGTTTGGATTTAATGCCAG, 1576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lightner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein, Theodore M.
Hubbard, Natalie L.
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                    DNA (genomic)
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No. 6376749el Starches via Modification
Expression of Starch Biosynthesis
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25
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                                                                                                                                                             74.0%;
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                                                                                                                                            Score 58.4; DB 4;
Pred. No. 1.4e-06;
0; Mismatches 26;
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                                                                                                                                                                               Length 2165;
                                                                                                                                                Indels
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RESULT 7 US-09-257-894-1

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LOCATION:
US-09-257-894-1
                                                                                                                              Sequence 14, Application US/08941445A Patent No. 6107060 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
APPLICANT: Keeliny,
APPLICANT: Guan, Hamping
APPLICANT: Guan, Harping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS:
ADDRESSE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: JUNE 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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o. 6376749
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Lightner, Jonathan
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Wlein, Theodore M.
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79..2476
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Pred. No. 1.6e-06;
0; Mismatches 26;
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Sequence 1, Application US/09087277B

Patent No. 6169226
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: LARSSON, Hakan
APPLICANT: LARSSON, Hakan
TITLE OF INVENTION: STARCH BRANCHING ENZYME II
FILE REFERENCE: 003300-486
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US-09-087-277-1
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APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-196
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
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CITY: Boulder
CHATE: CO
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NAME/KEY:
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LENGTH: 2725 base pair
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NAME/KEY:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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STRANDEDNESS:
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91..264
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265..2487
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Pred. No. 1.6e.
0; Mismatches
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                                                               POTATO
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RESULT 10
US-09-658-499-1
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NAME/KEY: misc feature
LOCATION: (2154)..(2156)
COTHER INFORMATION: Amino acid 608 is Xaa wherein
US-09-087-277-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
GENERAL INFORMATION:
APPLICANT: EK, BO
APPLICANT: KHOSNOOI
                                      Sequence 1, Application Patent No. 6469231
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                        Query Match
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NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides
OTHER INFORMATION: n wherein n
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NOCATION: (189)..(2825)
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NAME/KEY: misc feature
LOCATION: (1896)..(1898)

OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
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NAME/KEY: misc_feature
LOCATION: (1404)...(1406)
OTHER INFORMATION: Amino
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: (333)..(2825)
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LOCATION: (189)..(332)
FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION: Amino
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LOCATION: (285)..(287)
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                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                      1619
                                                                                                                         835
                                                                                                                                                                            775
 EK, Bo
KHOSNOODI,
                                                                                                                                                                                                     ACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGG 1678
                                                                                                                                                 AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                                                                                                                                                          ACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGG
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino a
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                                                                                                                                                                                                                                           2.7%;
 Jamshid
                                                                                                                                                                                                                                                                                                                                                                                                                         acid
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Pred. No. 2
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= A,
                                                                                                                                                                                                                                 Mismatches
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G or T.
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1
                                                                                                                             Matches
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (189)...(2825)
NAME/KEY: sig_peptide
LOCATION: (189)...(332)
NAME/KEY: mat_peptide
LOCATION: (333)...(2825)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR PELICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR PILING DATE: 1995-11-29
PRIOR FILING DATE: 1995-11-29
PRIOR FILING DATE: 1995-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: STARCH BRANCHING ENZYME FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: SE 9601506-0 PRIOR FILING DATE: 1996-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Nucleotides 92, (
OTHER INFORMATION: n wherein n = A,
NAME/KEY: misc feature
LOCATION: (285). (287)
OTHER INFORMATION: Amino acid -16 is
OTHER INFORMATION: or Fhe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism:beII gene OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino
                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1896)...(1898)
OTHER INFORMATION: Amino a
OTHER INFORMATION: or Phe-
                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino
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LOCATION: (1404)...(1406)
OTHER INFORMATION: Amino
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LOCATION: (92)..(2156)
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ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 3074
                              1679 AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
 835
                                                                                                                                            Similarity
AAGCTTTTTCTCGTGGTTATGAAAAAAATGGGTTTCACTCGTAG
                                                               ACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTT
                                                                                             ACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGG
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LARSSON, Hakan
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Pred. No. 2e-0:
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RESULT 11
US-09-257-894-5/c
; Sequence 5, Application U
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, K

US/09257894

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
                                                                                                                                                                    APPLICANT: SCHBIFLINGER, APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: ATA:
RIOR APPLICATION NUMBER: 09/
APPLICATION NUMBER: 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
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COUNTRY: USA
ZIP: 22313-0299
MPUTER READABLE!
                                                                  CITY: Alexandria
                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                         AACACTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGCCT 1230
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1007 Market Street
                                                                                    1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 302-992-4926
302-773-0164
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                                                                                                                     ADDRESS
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Pred. No. 1
                                                                                     Suite 500
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NUMBER OF SEQ ID NOS: 19335 SOFTWARE: PATENT.PM SEQ ID NO 2813 LENGTH: 832

ORGANISM: Homo sapiens

TYPE: DNA

CURRENT APPLICATION NUMBER: US/0 CURRENT FILING DATE: 2000-07-21

FILE REFERENCE: GENSET.054PR2

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S. APPLICANT: Giordano, J.)
TITLE OF INVENTION: ESTS

and Encoded Human Proteins.

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                           RESULT 13
US-09-621-976-2813
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Sequence 2813, Application US/09621976 Patent No. 6639063
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Best Local 9
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
(IOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
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                                                                                                              1147 AAAACCAGGAGATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGA 1197
                                                                                                                                                                                                                                                             967
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US-09-621-976-2813

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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyt
; NAME/KEY: unsure
; LOCATION: 125-126
; OTHER INFORMATION: a, t,
US-09-313-294A-3795
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLY
FILE REFERENCE: PL-00.7 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 3795
LENGTH: 279
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US-09-313-294A-3795
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Patent No. 6476212
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                            Similarity
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                                 CCCTAATCGGCGATGGCGACGGTGGCGATGGACATCTCGAAGCCCACTCCAGTGGCGTCC
GGCGACGAGGCCGCGGCGGCCAAGGGGANNAGCGGCGGAGGGGGCGAGGGGCTGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 1.9%; Score 41.2; DB 4; Length 364; Local Similarity 11.2%; Pred. No. 0.049; hes 31; Conservative 131; Mismatches 114; Indels
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                                                                                  WYMRASMKKSKYCAWSRKGSKCCMYSRKGSKSCYCC
                                                                                                                           TCCTCTGCGCGCGCATGGCCTGTTCGATGCTGTTCC 368
                                                                                                                                                                   GMMSSMYGASKRMSSMCSASTRMSSÅSCMMYMMMSAGSYASCAWKMSKYRRCAKWSCTYS
                                                                                                                                                                                                         TCCTCTCGTACGCCTCGCTCTCTCGAATCTCCCCCGTCTGGCTTTGGCTCCCCCTTCTCTC
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Score
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1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

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7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

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10621.793 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd
12 US-10-434-893A-3

12 US-10-434-893A-1

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9 US-09-792-127-3

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12 US-10-424-893A-4

9 US-09-792-127-1

12 US-10-424-599-130848

US-09-938-842A-337

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Sequence 3, Appli
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Sequence 3, Application US/10434893A

Publication No. US20040060083A1

GENERAL INFORMATION:

APPLICANT: Ahmed Regina
APPLICANT: Sadequr Rahman

TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and star

FILE REFERENCE: 69425

CURRENT FILING DATE: 2003-05-09

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 2.1

SEQ ID NO 3

LENGTH: 11476

TYPE: DNA

ORGANISM: Aegilops tauschii
FEATURE:

NAMB/KEY: MISC FEATURE

LOCATION: (1)...(11476)

OTHER INFORMATION: n is a, c, g or t
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FEATURE:

OTHER INFORMATION: SSBEIIa gene

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2147; Conservative 0; Mismatches
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15 US-10-056-454A-12
19 US-09-938-842A-872
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17 US-10-345-072-87
18 US-10-123-156-10
19 US-10-146-731-10
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Result No.

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	 GAACA 207	18 TGCTATTTTTCGTGCTGTAGATACCTGAAGATATCGA	מם
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	TGCAT 1957	AGCCTTGGCCCCGTGCTGGCTCTTGGGCCACTGAAAAAATCAGATGGAT	Вb
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	CGTGC 17	18 AGAGNGACGACTTGGCAAGTCCGGCGCAACCTGAAGAATTACAGGTACACACAC	qa
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	2660 1	1658 TTGCAGGCCGTCCTGAGCCGCCGCCGCCTCCAGGAAGGTCCTGGTGCCTGA	da
 	· O	сядасассатсствя в советствення в применения в	γQ
	GCATT 16	98 CIGITCTIGCIGIAACIGCAAGITGIGGCGITTTITCACIATIGIAGIC	đđ
	GCATT 600	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	γŞ
 	CITC 15	38 ACCACG	Db ,
	CTTC 54	CACGGCTTTGATCATTCCTCGTTTCATTCTGATATAT	ş
	15	78 CTGAACCTGTATTTTTTCCCCCGCGGGGAAATGCGTTAGTGTCACCCAGGCCCT	Db ·
	GIGIT 480	1 CTGAACCTGTATTTTTTCCCCCGCGGGAAATGCGTTAGTGTCACCCAGGCCCT	Ş
	GCTTC 14	18	Db a
 	റ്റ	GTTCCCCAATTGATCTCCATGAGTGAGAGAGATAGCTGGATTAGGCGATC	Q
	GA	1358 CTCCCCGTCTGGCTTTGGCTCCCCTTCTCTCTCTGCGCGCGCATGGCCTGTTT	đđ
	TCGAT 360	01 CTCCCCGTCTGGCTTTGGCTCCCCTTCTCTCTCTCTGCGCGCGCATGGC	ν.
	CGAAT 1357	241 ACTICCONCINCTON CAGGANGANGUACIO CICCUMACGOCICGONICION 1298 ACTICCOGTOGOTOCTOCAGGANGANGGACTCOTOTOGTACGCOTOGOTOTOTO	8
	3GCGG 12	38 GTGTGGCGCGGGCCGGCGTCGGAGTGGCGGGGCCGGACCGGAGCGGAGGG	, p
	GGGCGG 240	1 GTGTGGCGCGGCCGGCGTCGGAGTGGCGCGGGCCGGCTCGGAGCGGAGGGGCC	δ
	TCTCG 1237	1178 CTGGCTGACTCAATCACTACGCGGGGATGGCGACGTTCGCGGTGTCCGGCGCGAC	90
	-1	GCTGACTCAATCACTACGCGGGGATGGCGACGTTCGCGGTGTCCGGGCGA	8
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3158
1980
1920 CTC 2978 CTC
1860 ATT 2918 ATT
QY 1800 TTITCCCCTCTCTTTTTCCAGTGCTGAAGGTATCGTCTAATTGCATATCTTATAAGAAA 18 Db 2858 TTITCCCCCTCTCTTTTTCCAGTGCTGAAGGTATCGTCTAATTGCATATCTTATAAGAAA 29
17 27
16 27
16 26
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15 25
2 4 4
13 24
23
Qy 1260 GGTCCTTTCATCATGCAAATTTTGGGGAACATCAAAGAGAGAAGACTAGGGAACACATT 131
12

RESULT 2
US-10-434-893A-1
; Sequence 1, Application US/10434893A
; Publication No. US20040060083A1
; GENERAL INFORMATION:
; APPLICANT: Ahmed Regina
; APPLICANT: Matthew Kennedy Morell
; APPLICANT: Sadequr Rahman

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US-10-434-893A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10434893A publication No. US20040060083A1 GENERAL INFORMATION:
APPLICANT: Ahmed Regina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 2780
                                                                                                                                                                                                                                                                        Matches 140;
                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and :
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTMARE: Patentin version 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and star
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SSBEIIb cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                 1130
                                                                                                                                                                                                                     1010 GAAGTGAACATGACAGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGC 1069
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                                                                         358 ACTGAAGAAATTGATGCTGAAGGCGTGAGCAGAATGGACAAAGAATCATCCACGGTGAAG
                                                                                                                                                                       298 GAACCAAGCCTGCACGATGGAGGTGAAGATACTATTCGGTCTTCAGAGACATATCAGGTT 357
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AAACCGCGAGTTGTCCCAAAACCAGGAGATGGGCAGAAATATATACGAGTTGACCCAACA 1189
                                                                                                                          ATTGTGGAAACAATCACTGATGGTGTAACCAAAGGAGTTAAGGAACTAGTCGTGGGGGAG 1129
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Pred. No. 3.6e-48;
0; Mismatches 16;
                                                                                                                                                                                                                                                                   Score 90.8; DB 12;
Pred. No. 2.9e-15;
0; Mismatches 82;
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US-09-792-127-3
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10434893A Publication No. US20040060083A1 GENERAL INFORMATION:
                                                                                                                                              SOFTWARE: PatentIn version 2.1 SEQ ID NO 4
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Best Local Similarity
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APPLICANT: Allen, Steve
APPLICANT: Beckles, Diar
APPLICANT: Butler, Karla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 136;
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SEQ ID NO 3
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Patent No. US20020002713A1
                                                                                                                                                                                       TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and start TITLE OF INVENTION: containing products with an increased amylose content FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
RUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadegur Rahman
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TYPE: DNA
ORGANISM: Triticum aestivum
  NAME/KEY: MISC_FEATURE LOCATION: (1)...(6550)
                                                                       TYPE: DNA ORGANISM: Aegilops tauschii
                                                  FEATURE:
                                                                                                                          ENGTH: 6550
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Butler, Karla
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Pred. No. 2.5e-13;
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OTHER INFORMATION: FEATURE:

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APPLICANT: Beckles, Diane M.
APPLICANT: Beckles, Diane M.
APPLICANT: Beckles, Rich
TITLE OF INVENTION: Starch Branching Enzyme III
FILE REFERENCE: BB1439 US.
CURRENT APPLICATION NUMBER: US/09/792,127
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/186098
PRIOR TILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Office 97
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; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-1
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Best Local (
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                                                                                                            Sequence 130848, Application US/10424599 
Publication No. US20040031072A1 
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 81; Conserv
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                                    APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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CANT: Zhou Yihua
CANT: Cao Yongwei
CANT: Cao Yongwei
OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                            1123
                                                                                                                                                                                                                                                                                            1183 CCCAACACTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGCCTA 1231
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Similarity 61.4%;
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                                                                                                                                                                                                                                                       CCCAACGCTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTA 113
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%;
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Pred. No. 2e-12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64.2; DB 9;
Pred. No. 2.2e-07;
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRICA APPLICATION NUMBER: US 60/227,866
PRICA REPLICATION NUMBER: US 60/264,647
PRICA FILING DATE: 2001-01-16
PRICA FILING DATE: 2001-01-16
PRICA FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 337
LENGTH: 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
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SEQ ID NO 130848
LENGTH: 470
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: PAT_MRT3847_89163C.1
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                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                         Local Similarity
nes 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1548 TGTGGCCTTTTTGTTTTGGGGAAAACACATTGCTAAATTCGAATGATTTTGGGTATACCT 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 TTTTGCACTTTTGATACCTACTATACTGTAAATTTATAACGTAAATTTTTTAAAATGCTA
                                                                                                                  1619 АСАGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGG 1678
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                                     AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG
                                                                                 ACCGATATGGGCAGTACAGAAAACTGCGTGAAGAATTGACAAGAATGAAGGTGGTTTGG
    AGGCATTTTCTCGTGGTTATGAAATATTTGGCTTCACTCGAAG 629
                                                                                                                                                            Conservative
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73.8%;
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Pred. No. 9.2e-08;
0; Mismatches 74
                                                                                                                                                            0;
                                                                                                                                                              Score 59.8; DB 9;
Pred. No. 4.5e-06;
0; Mismatches 27;
                                                                                                                                                                                                     Length 2577;
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RESULT 9
US-09-938-842A-337
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-337
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Publication No.
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                           APPLICATION NUMBER: US/10/056,454A FILING DATE: 25-Jun-2002 INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 20
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
ATREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: National Starch and Chemical Investment Holding Corporation TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1619
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                STATE: Delaware COUNTRY: United States of America ZIP: 19720
                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                          LENGTH: 3231 base pairs
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o. US20040009476A9
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  DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US20030166919A1
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Pred. No. 4.5e-06;
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 130849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 130849, Application US/10424599
Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 73.8 Matches 76; Conservative
                                                                                                                                                             Matches
                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                             LENGTH: 5164
TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                             Local
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                                 1680 AGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                                                                                                   1620 CAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGGA 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 ACAGGTATTCACAGTACAAGAAAATGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                874 AAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAG 916
                                                                           927 CCGTTATGGACAATACAAAAGATTGTGTTATGAAATTGACAAGCATGAAGGCGGTCTGGA
987 TACATTTTCTCGTGGTTATGAAAAATTTGGCTTCATACGCAG
                                                                                                                                                                           2.7%;
Similarity 73.5%;
                                                                                                                                                           Conservative
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                                                                                                                                                           Score 58.8; DB 1:
Pred. No. 1.5e-05
0; Mismatches 2:
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RESULT 12
US-10-397-954A-1
(Sequence 1, Application US/10397954A)
(Sequence 1, Application US/10397954A)
(Publication No. US20030221220A1)
(Publication No. US20030221220A1)
(Publication No. US20030221220A1)
(Publication No. US20030221220A1)
(Publication No. Rainer E. Applicant: Broglie, Karen E. Applicant: Broglie, Karen E. Applicant: Hines, Christopher F. Applicant: Naize Starch Containing Elevated Amounts of Actual Amylose FILE OF INVERTION MAIZE STARCH CONTAINING Elevated Amounts of Actual Amylose CURRENT Application NUMBER: US/10/397,954A
(CURRENT Application NUMBER: US/10/397,954A
(CURRENT Application NUMBER: 60/368,387
(PRIOR Application NUMBER: 60/368,387
(PRIOR Application NUMBER: 60/368,387
(PRIOR Application NUMBER: 60/381,534
(PRIOR FILING DATE: 2002-03-27
(PRIOR Application NOS: 6
(SOFTWARE: Microsoft Word 97
(SEQ ID NO )
(LENGTH: 2443
(PRIOR Attificial Sequence PRATURE: NAME/KEY: misc_feature
(PCATION: (1).~(2443))
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Query Match

2.8%;

Score 59.8;

DB 14;

Length 3231;

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Sequence 1, Application US/10397954A
Publication No. US20030221220A1
GENERAL INFORMATION:
APPLICANT: Pearlstein, Richard W.
APPLICANT: Broglie Karen E.
APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Electric File Reperence: BB1510 US NA
CURRENT APPLICATION NUMBER: US/10/397,954A
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR FILING DATE: 2002-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
LOCATION: (1). (2443)
; OTHER INFORMATION: SBEII modified region
US-10-397-954A-1
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                                                                                                                                                                                                                                               US-10-056-454A-17; Seguence 17, Application US/10056454A; Publication No. US20030166919A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6
SOFTWARE: Microsoft Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/381,534
PRIOR FILING DATE: 2002-05-16
                                                                                                        GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: National Starch and Chemical Investment Holding Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 2443
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                                                                                                                                                                                                                                                                                                                                                                                                                  CATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
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                                                          CITY: Newcastle
STATE: Delaware
                                                                                                  STREET: 1000 Uniqema Blvd.
                                       COUNTRY: United States
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READABLE FORM
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Pred. No. 1.
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Pred. No. 1.1e-05;
0; Mismatches 26;
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SEQUENCE DESCRIPTION: SEQ ID NO: US-10-056-454A-17
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SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2520 har-
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STRANDENNESS: single
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TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-056-454A-16
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                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
RADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
        1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: National Starch and Chemical Investment Holding Corporate OF INVENTION: Improvements in or Relating to Plant Starch NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1679 AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                                                                      1619 ACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGG 1678
                                                508 ACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19720
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                                                                                                                                                                                                                                                                                                                          LENGTH: 2576 base pairs
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Pred. No. 1.3e-05
0; Mismatches 2
                                                                                                                                    Score 58.2; DB 14;
Pred. No. 1.3e-05;
0; Mismatches 28;
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AAGCTTTTTCTCGTGGTTATGAAAAATGGGTTTCACTCGTAG 610

Search completed: April 10, 2004, 20:07:30 Job time : 766.289 secs

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Title:
Perfect score:
Sequence:
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Listing first 45
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1 (bases 1 to 623)

Tingey, S. V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.

DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                 CA726861 623 bp mRNA linear EST 26-NOV-2002 wdelf.pk002.g8 wdelf Triticum aestivum cDNA clone wdelf.pk002.g8 5' end, mRNA sequence. CA726861 CA726861 GI:25448761
                                                                                                                                                                                                                                                          Triticum aestivum
                                                                                                      Crop Genetics
                                                                                                                                                                                                                                                                       Triticum aestivum (bread wheat)
                                           I. DuPont de Nemours and Company
Innovation Way, P.O. Box 6104, Newark,
el: 302-631-2602
ax: 302-631-2607
               il: Scott.V.Tingey@USA.dupont.primer: M13.
      Location/Qualifiers
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Result No.

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                                                                                                             Plate:
Seq pri
                                                                                                                               Email: scloutier@agr.gc.ca
was cloned directionally, not all
primer were from the 5' end (same
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Plate: 031 row: H column: 05
                                                                                                                                                                                                                                                                                                                                                                           Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                   Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture
195 Dafoe Rd, Winnipeg, MB, Canada R
Tel: (204) 983-2340
Fax: (204) 983-4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ239365
BQ239365.1
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/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI, Wheat (Triticum aestivum, Hi Line) developing
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                                                                                                                                                                                                                                        Tel: 33 1 69 47 54 00

Tax: 33 1 69 47 54 00

This sequence has been generated in the framework of the french plant genomics programme 'Genoplahte' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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     Score 235; DB 14;
Pred. No. 1.9e-39;
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after po SK+; Si d of cDN). Due t cases t cases t cases t in set ge inser	Fax: 039482-5522 Fax: 039482-5595 Email: stein@ipk-gatersleben.de Insert Length: 577 Std Error: 0.00 Plate: 52 row: D column: 11 Seq primer: M13rev. FEATURES Seq primer: M13rev. 1577 FOATURES 1577 Source /organism="Hordeum vulgare subsp. vulgare"	POOIDEAE; Triticeae; Hordeum. REFERENCE 1 (bases 1 to 577) AUTHORS Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U. TITLE Barley ESTs from developing seeds JOURNAL Unpublished (2002) COMMENT Contact: Stein Nils Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstr. 3, 06466, Gatersleben, Germany	CA025454 LOCUS LOCUS LOCUS DEFINITION LESSION LESSION LESSION LESTION	Matches 241; Conservative 0; Mismatches 10; Indels 0; Gaps 0; 978 AGATACCTGAAGATATCGAGGAGCAAACGGCGGAAGTGAACATGACAGGGGGGACTGCAG 1037 pb 243 AGATACCTGAAGACATCGAGGAGCAAACGGCGGAAGTGAACATGACAGGGGGGACTGCAG 302 97 1038 AGAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGTAA 1097 pb 303 AGAAACTTGAATCTTCAGAACCGACTCAAGGCATTGTGGAAACAATCACTGATGGTGTAA 362 27 1098 CCAAAGGAGTTAAGGAACTAGTCGTGGGGAGAAACCACTGATGGTGTAA 362 28 1098 CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGATTGTGGAAACCACGAGAGTAACCAGGAG 1157 29 1158 ATGGGCAGAAAATATATACGAGATTGAGCGAGAAACCGCGAGTTTTCGGAAGCATCTTGACT 1217 29 1158 ATGGGCAGAAAATATATACGAGATTGACCCAACGCCAAAACCGCGAGTTTTCGGAAGCATCTTGACT 1217 29 1218 ACCGGTAATGC 1228 29 1218 ACCGGTAATGC 1228 29 1218 ACCGGTAATGC 493 RESULT 4
source 1. 412 /organism="Hordeum vulgare subsp. vulgare" /oultivr="barke" /cultivr="barke" /sub species="vulgare" /db_xref="caxon:112509" /db_xref="taxon:112509" /clone="ht264118" /fissue_type="pericarp" /dev_stage="0-7 DAP (days after pollination)" /clone lib="HZ" /cl	Institute of Plant Genetics and Croy Institute of Plant Genetics and Croy Corrensetr 3, 06466, Gatersleben, Crel: 039462-5522 Fax: 039462-5525 Fax: 039462-5525 Email: stein@ipk-gatersleben.de Insert Length: 412 Plate: 64 row: I column: 18 Seq primer: M13rev	ORGANISM HOXDeum vulgare subsp. vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. REFERENCE 1 (bases 1 to 412) AUTHORS Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U. TIȚLE Barley ESTa from developing seeds JOURNAL Unpublished (2002) Conment Contact: Stein Nils Contact: Stein Nils	N ON	Query Match Best Local Similarity 93.2%; Pred. No. 4.6e-37; Matches 234; Conservative 0; Mismatches 17; Indels 0; Gaps 0; Matches 234; Conservative 0; Mismatches 17; Indels 0; Gaps 0; Qy 978 AGATACCTGAAGATATCGAGGAGCAAACGGCGAAGTGAACATGACAGGGGGGACTGCAG Db 307 AGGTACCTGAAGATATCGAGGAGCAAATGACGAGTGAAACATGACAGGGGGGGG

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Anderson,O.D., Chao,S., Crossman,C., Langridge,P., Lazo,G.R., Pham,J., Rausch,C.J., Sutton,T., Woo,J. and Wilson,C.
The structure and function of the expressed portion of the wheat genomes - Meiotic anther cDNA library
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EST.
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US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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                                                                                                                                                                                                                                                                                                                                                                                           Email: oandersn@pw.usda.gov
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                                                                                                                                                                                         /organism="Triticum aestivum"
/mol type="mRNA"
/cultivar="Chinese Spring"
/db xref="teaxon:4565"
/clone="WHE4023_D10_H19"
/tissue_type="Anther"
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/dev stages meiotic stages pre-meiosis-metaphase I"
/lab host="E, coli DH10B"
/clone lib="Wheat meiotic anther cDNA library"
/note="Vector: pSPORTI; Site_1: SalI; Site_2: NotI; Plants
were grown in a glasshouse. Anther meiotic stage was
determined by removing anthers from individual primary
florets. One anther was sacrificed for microscopic
staging, and if determined to be between (and including)
meiotic stages pre-meiosis and metaphase I, the remaining
two anthers were collected and pooled for library
construction. The tissue, total RNA, and poly(A) RNA were
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Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudi
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh,
Development of Barley Transcriptome Resources
Unpublished (2001)
On Feb 1, 2002 this sequence version replaced gi:
Contact: Waugh R, Marshall DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM441043 219 bp mRNA linear EST 23-J
EBed02_SQ002_E01_R endosperm, 8 DPA, no treatment, CV Optic,
Hordeum vulgare subsp. vulgare cDNA clone EBed02_SQ002_E01 5
                                                                                                                                                                                                                                                                                                                                                                                                 Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 SDA, Scotland
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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1 (bases 1 to 219)
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                                                                                          /mol type="mRNA"
/mol type="mRNA"
/mol type="optic"
/sub species="vulgare"
/db xref="taxon:112509"
/clone="EBed02_SQ002_E01"
/tissue_type="endosperm"
/dev_stage="8_DPA"
/lab_host="DH10B"
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note="Vector: psport1; Site 1: Sal I; Site 2: Not I; Note="vector: psport1; directionally cloned into psport1
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85.6%;
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clone OSIIEB05120 5', mRNA sequence.
CB629365
CB629365.1 GI:29624354
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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1 (bases 1 to 831)

"Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
"Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
"Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
"Jantasuriyarat, Shou,B., Shou,B., Mazur,E.,
"Large-scale identification of ESTs involved in the interaction
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Biological Sciences West, 448A,
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PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq
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Fax: 520 621 9288
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BACKWARD: gga aac agc tat gac cat g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arizona Genomics Institute
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/dev_stage="3 week"
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                                                                                                                                                                                                                                                                                         /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
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Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG421022 1006 bp DNA linear GSS 22-ZMMBBC0034G11f ZMMBBC (ECORI) Zea mays subsp. mays genomic ZMMBBC0034G11 5', genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Zea mays subsp. mays
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CG421022.1
                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                      190 Frelinghuysen Road, Piscataway,
Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dr.Joachim Messing's lab
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Bharti, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2003)
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                            TGGGTATACCTCGGTGGATTCAACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATT 1656
TTGGTTTGCCTTTGTGGATTCAACAGATACAGTGAATATAAGAGATTACGTGCGGCTATT
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                                                               6.1%; llarity 60.1%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       bharti@waksman.rutgers
                                                                                                                                                                                                                                                     organism="Zea mays/mol_type="genomic [
cultivar="B73"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                  /clone="ZMMBBc0034G11"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBc (EccRI)"
/note="Vector: pTARBAC2.1; '
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Pred. No. 2.9e
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BQ754975.1
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BBed02_SQ003_F18_R endosperm, 8 DPA, no ti
Hordeum vulgare subsp. vulgare cDNA clone
                                                                                                                                                                                                                                                                                                   Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R. Development of Barley Transcriptome Resources Unpublished (2001)
                                                                                                                                                                                            Invergowrie, Dundee, DI
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                 Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotlan
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                    Contact: Waugh R, Marshall DF
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                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 189)
                                                                                                                                                                               est@scri.sari.ac.uk.
/sub_species="vulgare"
/db_xref="taxon:112609"
/clone="Ebedoz_20003_F18"
/tissue_type="endosperm"
/dev_stage="8_DPA"
                                                                                                                                                                                                                                                                                                                                                                                              Triticeae; Hordeum.
                                                                                                                                                        ocation/Qualifiers
                                                                                      cultivar="Optic"
                                                                                                           HOH!
                                                                                                                        organism="Hordeum
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                                                                                                       _type="mRNA"
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The structure and function of the expressed portion of the wheat genomes - 20-45 DAP spike cDNA library
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WHE0855_F05_K09ZS Wheat 20-45 DAP spike cDNA library Triticum
aestivum cDNA clone WHE0855_F05_K09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                guality sequence with phred score less than Seq primer: Stratagene SK primer. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE590829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: oandersn@pw.usda.gov
Sequence have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800 Buchanan Street, Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pooideae; Triticeae; Triticum.
1 (bases 1 to 342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGGCGGGCTGGACTTGCCGTCGCTCACGAAGAAGAAGACTCCTCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cione_lib="endosperm,
EBed02"
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/clone_lib="endos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene Function) project.
/clone="WHE0855 F05 K09"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/lab host="E_coll SOLR"
/lab host="E_coll SOLR"
/clone_lib="Wheat 20-45 DAP spike cDNA library"
/clone_lib="Wheat 20-45 DAP SPIKE cDNA library"
/note="Vector: Lambda Uni-ZAP XR excised phagemid;
/note="Vector: Lambda Uni-ZAP XR excised phagemid;
Site 1 ExcRI, Stite 2: Xhol; Plants were grown in t.
Site 1: ExcRI, Stite 2: Xhol; Plants were grown in t.
                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                     /cultivar="Chinese Spring"
/db_xref="taxon:4565"
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87.9%;
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Pred. No. 1.6e-14;
0; Mismatches 17
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20
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ORIGIN

were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

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RESULT 12
BU996927
LOCUS
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AUTHORS
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JOURNAL
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Best Local Similarity
Query Match
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
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HI06F01r HI Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
EU996927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: stein@ipk-gatersleben.de
Insert Length: 517 Std Error: 0.00
Plate: 6 row: F column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPX)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
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1 (bases 1 to 517)

Zhang, H., Weschke, W., Michalek, W., Stein, N.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            039482-5595
                                                                                             /tissue_type="female inflorescences"
/dev_stage="female inflorescences (approx. 3 mm in size)"
/lab_host="%X10-Gold"
/lab_host="%X10-Gold"
/clone_lib="HI"
/clone_lib="HI"
/clone_lib="HI"
/clone_tib="li"
/cl
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/clone="HI06F01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sub_species="vulgare"
/db_xref="GABI:250791"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Hordeum vulgare subsp. vulgare"
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Pred. No. 1e-10;
0; Mismatches 3;
      Score
      98.6;
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vulgare
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      13;
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cDNA clone HI06F01
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      Length
      517;
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BQ240653
LOCUS
      VERSION
KEYWORDS
SOURCE
                                                                                                           ACCESSION
                                                                                                                                                                             DEFINITION
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sequence. BQ240653

BQ240653 TaE05014F06R TaE05

Triticum aestivum

cDNA clone TaE05014F06R,

linear

EST 03-MAY-2002

568 bp

BQ240653.1 GI:20436529 BST. Triticum aestivum (bread wheat)

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KEYWORDS
SOURCE
ORGANISM
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AV913706
LOCUS
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AUTHORS
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                         1617 CAACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATT
                        1677 GGAAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                                                                                                                           101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 CTACCGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATT
 81 GGAAGTTTTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG
                                                                    21 CTACCGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 556)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Optice:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           germination shoots Hordeum v
bags23a09 5', mRNA sequence
AV913706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV913706 X. Sato unpublished cDNA library, germination shoots Hordeum vulgare subsp. v
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV913706.1 GI:18209483
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tadasu Shin-i
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACAGATACAGGGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAGTTTTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCCGCAG
                                                                                                                                         4.6%;
ilarity 96.2%;
Conservative
                                                                                                                                                                                                                                                                                                    /mol type="mRNA"
/culfivar="Haruna Nijo"
/sub species="vulgare"
/db xref="taxon:11509"
/clone="bags23a09"
                                                                                                                                                                                                                               /dev_stage="germination"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo germination shoots"
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Hordeum vulgare
                                                                                                                                                                                                                                                                                         tissue
                                                                                                                                                                                                                                                                                       type="shoots"
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D; Mismatches 4
                                                                                                                                             Score 98.6; DB 9;
Pred. No. 2.4e-10;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                               subsp. vulgare"
                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear EST 18-JAN-2002
, cv. Haruna Nijo
vulgare cDNA clone
                                                                                                                                                                               Length 556;
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AUTHORS
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                                                                      COMMENT
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Best Local Similarity
Matches 101; Conserv
                                                                                                                    TITLE
                                                                                                                                                                AUTHORS
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was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 014 row: F column: 06
                                                                                       1 (bases 1 to 139)
Hedley.P., Liu,H., Caldwell,D., McCallum,N., Mudie,S.,
Ramsay,L., Machray.G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
                                                                                                                                                                                                  Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cernact: Octro, Sylvie Cloutier
Cernact: Dr. Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 SDA, Scotland
                                                                                                                                                                                                                                                                                                                                                                                                                BM368073

139 bp mRNA linear EST 23-JUL-2002
EBed01_SQ002_B11_R endosperm, 6 DPA, no treatment, cv Optic, EBed01
Hordeum vulgare subsp. vulgare cDNA clone EBed01_SQ002_B11 5', mRNA
                                                                                                                                                                                                                                                                                                                           EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="TaE05"
/note="Vector: pspORT-P (Invitrogen Technologies); Site_1:
NotI; Site_2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="TaB05014F06R"
/tissue_type="developing seeds"
/dev_stage="5 days after anthes
/lab_host="2. coli DH10B"
/clone_lib="TaB05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Triticum aestivum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Glenlea"
/db_xref="taxon:4565"
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96.2%;
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Pred. No. 2.4e-10;
    Scotland,
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Search completed: April 10, Job time: 5678.27 secs
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Best Local &
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                                                                         121 TCG 123
                                                                                                                                                                                     218 CTCGGAGCGGAGGGGGGGGGGACTTGCCGTCGCTGCTCCTCAGGAAGAAGAACTCCTC 277
                                                                                                                                                                                                                                                        278 TCG 280
                                                                                                                                                  61 CTCGGAGCGGAGGGGCGGACTTGCCGTCGCTGCTCAGGAAGAAGGACTCCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          All sequence has a Phred quality score of 20 or over Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@scri.sari.ac.uk
                                                                                                                                                                                                                                GETETCCGGCGACCCTTGGTGTGGCGCGGGGCGCGCGGCGAGCGCTGCCGCGATCCGG
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pspORT1; Site 1: Sal 1; Site 2: Not 1; Non-normalised library, directionally cloned into pspORT1. Derived from endosperm tissue dissected from developing grains (6 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
                                                                                                                                                                                                                                                                                                                                                                                                   Gene Function) project."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="endosperm, 6 DPA, no treatment, cv Optic,
EBed01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="endosperm"
/dev_stage="6 DPA"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:112509"
/clone="EBed01_SQ002_B11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
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                                                                                                                                                                                                                                                                                                                         90.28;
                2004,
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                                                                                                                                                                                                                                                                                                                         Score 92.6; DB 12
Pred. No. 3.7e-09;
                    14:06:19
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No.
                                        GenEmbl:*

1: gb ba:*
2: gb htg:*
3: gb in:*
4: gb om:*
6: gb pat:*
7: gb pt:*
9: gb pr:*
10: gb sy:*
11: gb sy:*
12: gb sy:*
13: gb un:*
14: em ba:*
15: em ba:*
16: em fun:*
18: em in:*
18: em ov:*
19: em ov:*
11: em ov:*
11: em ov:*
11: em ov:*
12: em ba:*
13: gb un:*
14: em hum:*
15: em fun:*
16: em fun:*
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19: em sts:*
19: em htg hum:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
the number of results predicted by chance to have a
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          REFEREN
AUTHO
TITLE
                                                                                                                                                                                                  RESULT 1
AX031271
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANII
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Db 6438 TCAAACGCGAGAGTGGCTTGAAGAATATATATTTCTTTCT	Oy 1441 ATTACTPCCACGGTGGTCCACGGCCATCATTGGATGGGGTTGTTCTACTC 1500 1	1201 GUILLAGUAGUE GUILLAGUAGUE GUILLAGUE GUILL	1141 CTTAGGACAATCTAGAACTTCAATCAATCTGGATCAGAGGAACATCAAATATAGAGAAGTTTGA 1141 CTTAGGACAATCTAGAACTTCAATCAATTTTGGATCAGAGGAACATCAAATATATAGA 120 CTTAGGACAAATCTAGAACTTCAATCAATTTTGGATCAGAGGGAACATCAAATAATATAGA 120 CTTAGGACAAATCTAGAACTTCAATCAATTTTGGATCAGAGGGAACATCAAATAATATAGA 120 TAGGACAAATCTAGAACTTCAACAAAAAAATCAGACCTTGTCACCAATAATATAGAACATC 120 TAGATGTCAACACTTCAACAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 120 TAGATGTCAACACTTCAACAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 130 TAGATGTCAACACTTCAACAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 131 TAGATGTCAACACTTCAACAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 131 TAGATGTCAACACTTCAACAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 131 TAGATGTCAACACTTCAACAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 131 TAGATGTCAACACTTCAACAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 132 TAGATGTCAACACTTCAACAAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 132 TAGATGTCAACACTTCAACAAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 132 TAGATGTCAACACTTCAACAAAAAAAATCAGACCTTGTCACCATATATGCATCAGACCATC 132 TAGATGTCACACTTCAACAAAAAAAATCAGACCTTGTCACCTTATATGCATCAGACCATC 133 TAGATGTCACACTTCAACAAAAAAAATCAGACCTTGTCACCTTATATGCATCAGACCATC 133 TAGATGTCACACTTCAACAAAAAAAAATCAGACCTTGTCACCTTATATGCATCAGACCATC 133 TAGATGTCACACTTCAACAAAAAAAATAAAAATAAAAAAAA	5598 841 5658 901 5718 961 5778 1021

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Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
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1. (bases 1 to 11475)
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                    /product="starch branching enzyme IIa"
/protein_id="ARX26821.1"
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RAVLSRAASGGKVLVPDGESDDLASPAQPEELOIPEDIEEGGTAEVANTGGTAEKLQSS
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EYKRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYREWAPGAKAALVCDENNWNP
NADTMTRDDYGVWEIFLPNNADGSSAIPHGSRVKIRMDTPSGVKDSISAWIKFSVQAP
GEIPFNGIYYDDPEEEKVVFGHPGRKRPESLRIYESHIGNSSAFEPKINSYANFRDEVL
PRIKKLGYNAVQIMAIQEHSYYASFGYHVTNFFARSSRFGTPEDLKSLIDEAHELGLL
VLMDIVHSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHWMDSRLFNYGSWEVLRELLS
NARWHLEEYKEDGFREDGVTSMYTHHGLQMTFTGNYGSFGFATDVDAVYLMLNND
NARWHLEEYKEDGFREDGVTSMYTHHGLQMTFTGNYGSFFGFATDVDAVYLMLNND
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/product="starch branching enzyme IIa"
join(1204. .1336,1664. .1761,2038. .2279,2681. .2779, 2018. .2999, 2018. .3389,4105. .418 2949. .2991,3144. .3203,3539. .3619,3703. .3819,4105. .418 2949. .2991,3144. .3203,3539. .3619,3703. .3819,4105. .686 7447. .7550,8392. .8536,5856. .9703,9839. .9939,10116. .10 10395. .10550,10928. .11002,11092. .11175)
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/chromosome="2"
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|mol_type="genomic DNA"
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                                 TTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTATCCATTGG
                                                                                                             GACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGATGCGGTAGT
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Zea mays subsp. mays (maize)
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; PACCAD
Spermatophyta; Magmoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 691)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-FEB-2003) Genetics, USDA-ARS, North
University, 3513 Gardner Hall, Box 7614, Raleigh,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY235709.1 GI:30014041
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AY235709
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                CCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACATTACTTCCACGGTGGTCCACG
                                                                   TTTGGTTTCATACCTTTAACTTTGCTTTTGTGTTACTTGCAGTCATGCGTCAAGTAATAC
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.tt,S.R., Wilson,L.M.,
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/number=13
536..668
/gene="ael"
/number=14
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277. .387
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/mol_type="genomic DNA"
/cultivar="NC260"
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/product="amylose extender starch-branching enzyme"
/protein_id="AAP03861.1"
/db_xref="GI:30014042"
/db_xref="GI:30014042"
/translation="HASSNTIDGINGFDGTDTHYFHSGPRGHHWMWDSRLFNYGNWEV
LRFILSNARWHLERYKFDGFRFDGVTSMMYTHHGLGVTFTGNFNEYFGFATDVDAVVY
LMFILSNARWHLERYKFDGTFTGDFTFTGNFNYTHHGLGVTFTGNFNEYFGFATDVDAVVY
LMILSNARWHLERYKFDAVTIGEDV"
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join(<61..190,277..387,536..>668)
/gene="ae1"
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/gene="ae1"
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/db_xref="taxon:4578"
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                                                                                                                                                                              Score 250.8; DB 8; Pred. No. 1.7e-40; 0; Mismatches 192;
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RESULT 4
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Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                   1 (bases 1 to 693)
Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY235691 693 bp DNA linear PLN 16-APR-200: Zea mays subsp. mays cultivar A6 amylose extender starch-branching enzyme (ael) gene, exons 12, 13, and 14 and partial cds.

AY235691
                                                                                          Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
                                                                                                                                                                                              2 (bases 1 to 693) Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S.
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/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
                                                                          Location/Qualifiers
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  ATTTTGGATTTGCTACTGATGTTGATGCGGTAGTTTACTTGATGCTGGTCAACGATCTAA 2002
                                                                                            TATTTTCTTTCTAAGTTTCTTCTTCTAGATGACATTTACTGGGGAACTATGGCGAAT 1942
                                                                                                                                                       ATATTTGTTATATATCATTCCTTCTTCTAATCTAAAGTCA---
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/product="amylose extender starch-branching enzyme"
/protein_id="AAP03843.1"
/db_xref="GI:30014006"
/translation="HASSNTLDGLNGFDGTDTHYFHSGPRGHHWMWDSRLFNYGNWEV
LRFILSNARWHLBEYKFDGFRFDGVTSMYYTHHGLQVTFTGNFNEYFGFATDVDAVVY
LMTLYNDLIHGLYFBAVTIGEDV"
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/db_xref="taxon:4578"
                                                    ------TGCATTTTACTTTAGGTAACATTTACGGGGAACTTCAATGAGT
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join(<61..190,277..387,536..>668)
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/gene="ae1"
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Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
Genetic diversity and selection in the malze starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY235701 693 bp DNA linear PLN 16-APR-200 Zea mays subsp. mays cultivar F2 amylose extender starch-branching enzyme (ael) gene, exons 12, 13, and 14 and partial cds.
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University, 3513 Gardner Hall, Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                      TTTGGTTTCATACCTTTAACTTTGCTTTTGTGTTACTTGCAGTCATGCGTCAAGTAATAC
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                                                                                                          Conservative
                                                                                                                                                                                                                                 536. .668
/gene="ael"
                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="hassntldglngfdgtdthyfhsgprghhmmmdsrlfnygnmev
lrfllsnarmmleeykfdgfrfdgvtsmmythhglqvtftgnfneyfgfatdvdavvy
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/gene="ae1"
                                                                                                                                                                                                                                                                               /gene="ae1"
/number=13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="amylose extender starch-branching enzyme"
protein id="pape03853.1"
/db_xref="GI:30014026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="mays"
/db_xref="taxon:4578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                           "MLVNDLIHGLYPEAVTIGEDV"
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                                                                                                          Mismatches
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x 7614, Raleigh,
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Submitted (13-FEB-2003) Genetics, USDA-ARS, North University, 3513 Gardner Hall, Box 7614, Raleigh, Location/Qualifiers
                                                                                                                                                                                                             1 (bases 1 to 712)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                     Direct Submission
                                                                                                                              Whitt, S.R.,
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                                                                                                                              Wilson, L.M.,
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                                                                                                                              Tenaillon, M.I., Gaut, B.S.
                                          Carolina State
NC 27695, USA
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                                                                                                                              and Buckler, E.S.
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TATTTTCTTTCTAAGTTTGTTTCTTGTTCTAGATGACATTTACTGGGGAACTATGGCGAAT 1942
                                                                                                                 CTAGTATGCTTGTACAATTTTACCTGATGAGATCATGGAAGATTGGAAGTGATTATTATT 1882
                                                                                                                                                                                                                             GCTATGCATCATAACATGTATCATGATCAGGACTTGTGCTACGGAGTCTTAGATAGTTCC 1822
                                                                                                                                                                                                                                                                                                                       ATGGATTACAAGTAAGTCATCAAGTGGTTTCAGTAACTTTTTTAGGGCACTGAAACAATT 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGACCTCCATGATGTATACTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAATTTTATCCGTATGCAGGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATATTCTATTCTTATGCAGGTATTGAGATTCTTACTGTCAAACGCGAGATGGTGGCTTG 1642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACATTACTTTCACAGTGGTCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGGTTTCATACCTTTAACTTTGCTTTTGTGTTACTTGCAGTCATGCGTCAAGTAATAC
                                                              ATATTTGTTATATATCATTCCTTCTTCTAATCTAAAGTCA-----
                                                                                                                                                                                                                                                                                            ÀCGGÀTTÀCÀÀGTÀATTTÀAGCTTTATGCCTGTTÀGTTTATCT-----TCÀCTTGCTA 429
                                                                                                                                                                                                                                                                                                                                                                                                        AGGAATATAAGTTTGATGGTTTCCGTTTTGATGGTGACCTCCATGATGTACACTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGGAACTGGGAAGTACG--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536. .668
/gene="ae1"
/number=14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number=12
277. .387
/gene="ae1"
/number=13
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gene="ae1"

product="amylose extender starch-branching enzyme"

join(<61. 190,277. .387,536. .>668)

join(<61. 190,277. .387,536. .>668)

join(<61. maylose extender starch-branching enzyme"

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/translation="HASSNTLDGLNGFDGTDTHYFHSGPRGHHWMWDSRLFNYGNWEV"
/translation="HASSNTLDGLNGFDGTDTHYFHS
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/mol_type="genomic DNA"
/cultivar="I205"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="ael"
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Pred. No. 1.7e-40;
0; Mismatches 192;
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Best Local Similarity
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AY235690
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Zea mays subsp. mays (maize)
Zea mays subsp. mays
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae, Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clac; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State
University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 713)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler, Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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     Conservative
                                                                                                                                            /number=12
277. 387
/gene="ae1"
/number=13
536. 668
/gene="ae1"
/number=14
                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=2
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/translation="HASSNTLDGLNGFDGTDTHYFHSGPRGHHWMWDSRLFNYGNWEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(<61. .190,277. .387,536. .>668)
/gene="ae1"
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/mol_type="genomic_DNA"
/cultivar="A272"
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                             12.2%;
Score 250.8; DB 8;
Pred. No. 1.7e-40;
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Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 713)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                                                                                                                         AY235692 713 bp DNA linear
Zea mays subsp. mays cultivar B103 amylose extender
starch-branching enzyme (ae1) gene, exons 12, 13, an
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Whitt,S.R.,
          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCATGGACTTTATCCTGATGCTGTATCCATTGGTGAAGATGTAAGTG 2050
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Location/Qualifiers
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Pred. No. 1.7e-40;
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/ Match 12.2%; Score 250.8; DB 8; Length 713; Iocal Similarity 65 1% Pred. No. 1 7e-40;		536668 /gene="ael" /number=14	27387 /gene="ae1" /number=13	61190 /gene="ael" /number=12	/product="anylose extender starch-branching enzyme" /protein_id="AAP03845.1" /db_xref="GI:30014010" /translation="HASSNTLDGLNGFDGTDTHYFHSGPRGHHWMDSRLFNYGNWEV /translation="HASSNTLDGLNGFDGTDTHYFHSGPRGHHWMDSRLFNYGNWEV LMLVNDLHHGLYPEAVTICEDV"	<pre>/ yeris</pre>		/organies of the property of t	Location/Qualifiers 1. 713 1. 713 1. 703 mays substitutes mays:	Direct Submission Direct Submission Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State Submitted, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA		1 (ban Whitt, Genetic Proc. 1	Zea mays subsp. mays (maize) Zea mays subsp. mays Zea mays subsp. mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACCAD clade; Pantcoldeae; Andropogoneae; Zea.	partial cds. AY235693 GI:30014009	AY235693 713 b Zea mays subsp. mays cultivar	2003 ITCATGGACTITATCCTGATGCTGTATCCATTGGTGAAGATGTAAGTG 2000	۱ »	521TĠCATTTTACTTTAGGTAACATTTACGGGGAACTTCAATGAGT 563 1943 ATTTTGGATTTGCTACTGATGTTGATGCGGTAGTTTACTTGATGCTGGTCAACGATCTAA 2002	
AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.	12244216	Genetic diversity and selection in the maize starch pathway Proc. Natl Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002) 22247734	REFERENCE 1 (bases 1 to 713) AUTHORS Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E.S.	ORGANISM Zea mays subsp. mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Liliopsida; Poales; Poaceae; PACCAD	extend 1d part	AY235694 713 bp DNA linear PLN 16-APR-2	624 TICATGGACTITATCCTGAGGCTGTAACCATTGGTGAAGATGTAAGTG 671	QY 1943 ATTTTGGATTTGCTACTGATGTTGATGCGGTAGTTTACTTGATGCTGGTCAACGATCTAA 2002	Db 521	Db 481 ATATTGTTATATATCATTCCTTCTTCTAATCTAAAGTCA	Db 430 AGTCTGACTGGAÁTACTGGAÍTATGCCTGGGÁACTÁGTTTTGTTTÁGÍATĆ 480 QY 1823 CTAGTATGCTTGTACAATTTTACCTGATGAGATTGTAAGAATTGGAAGATTGATT	377 1763	OY 1643 AAGAATATAAGTITGATGGATTICGATTIGATGGGGTGACCTCCAGGATGTATACTCACC 1702	OY 1583 GATATTCTATCCTTATGCAGGTATTGAGATTCTTACTGTCAAACGCGAGATGGTGGCTTG 1642	OY 1523 CTCTGACTTCTGTCACCATATTTGGCTAACTGTTCCTGTTAATCTGTTCTTACACATGTT 1582		14	OY 1343 TTCAGTTGCATCATCATCATCTGTGTACCCTGCAGTCATTCGTCAATAATAC 1402	461; Conservative 0; Mismatches 192; Indels 55; Gaps

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Submitted (13-FEB-2003) Genetics, USDA-ARS, North
University, 3513 Gardner Hall, Box 7614, Raleigh,
Location/Qualifiers
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                CTAGTATGCTTGTACAATTTTACCTGATGAGATCATGGAAGATTGGAAGTGATTATTATT 1882
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                                                    AGTCTGACTGGAATACTGGATTATGCCTGGGAACT----AGTTTTGTTTAGTATC
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Submitted (13-FEB-2003) Genetics, USDA-ARS, North
University, 3513 Gardner Hall, Box 7614, Raleigh,
Location/Qualifiers
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Zea mays subsp. mays

Ewaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;

Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae, PACCAD

clade; Panicoideae; Andropogoneae; Zea.
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Zea mays subsp. mays cultivar B73 amylose extender starch-branching
enzyme (ael) gene, exons 12, 13, and 14 and partial cds.
AY235695
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Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E.S.
Generic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Whitt, S.R., Wilson, L.M.,
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                                                  536. .668
/gene="ae1"
/number=14
                                                                                                      /gene="ae1"
/number=13
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/product="amylose extender starch-branching enzyme"
/protein_id="AAP03847.1"
/db_xref="GI:30014014" \
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join(<61. .190,277. .387,536. .>668)
/gene="ae1"
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|gene="ael"
|zene="ael"
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277. .387
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LRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVTFTGNFNEYFGFATDVDAVVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sub_species="mays"
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/cultivar="B73"
                                                                                                                                                                        gene="ael"
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NC 27695, USA
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Whitt,S.R.,
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AY235696
AY235696.1 GI:30014015
                                                                  1 (bases 1 to 713)
Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E. Genetic diversity and selection in the maize starch pathway proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                      Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Tenaillon, M.I.,
 Gaut, B.S.
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June 1. Submission
Submitted (13-FEB-2003) Genetics, USDA-ARS, North University, 3513 Gardner Hall, Box 7614, Raleigh, Location/Qualifiers
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     CTAGTATGCTTGTACAATTTTACCTGATGAGATCATGGAAGATTGGAAGTGATTATTATT
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                                  AGTCTGACTGGAATACTGGATTATGCCTGGGAACT------
                                                                     GCTATGCATCATAACATGTATCATGATCAGGACTTGTGCTACGGAGTCTTAGATAGTTCC
                                                                                                                                    ATGGATTACAAGTAAGTCATCAAGTGGTTTCAGTAACTTTTTTAGGGCACTGAAACAATT
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ilarity 65.1%;
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/number=13
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/gene="ae1"
/codon_start=2
/poduct="amylose extender starch-branching enzyme"
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LRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVTFTGNFNEYFGFATDVDAVVY
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/gene="ae1"
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/mol_type="genomic DNA"
/cultivar="B97"
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join(<61. .190,277. .387,536. .>668)
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/db_xref="taxon:4578"
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pred. No. 1.7e-40;
0; Mismatches 192;
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                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 713)
Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, B. Genetic diversity and selection in the malze starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays subsp. mays (maize)
Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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itt,S.R., Wilson,L.M.,
            536. .668
/gene="ael"
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                                                                                                                                                                                                                                                                                                                           /sub_species="mays"
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/cultivar="CI187-2"
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                                                                                                                          TTCATGGACTTTATCCTGAGGCTGTAACCATTGGTGAAGATGTAAGTG
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Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA Location/Qualifiers
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/gene="ae1"
/number=14
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/number=12
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LMLVNDLIHGLYPEAVTIGEDV"
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/cultivar="CML254"
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Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

[ (bases 1 to 713)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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starch-branching enzyme (ae1) gene, exons 12, 13, an
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/cultivar="IDS28"
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'gene='se1"

'product='amylose extender starch-branching

join(<61. .190,277. .387,536. .>668)
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DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
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Starch branching enzyme II (SBE II)
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DE Starch branching enzyme; starch solution of the solution 
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                                                                                                                                                                               New isolated cereal plant enzyme genes used for, earntisense sequences of granule bound synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS; starch branching enzyme; starch soluble synthase; debranching enzyme; endosperm; wheat; barley; granule-bound synthase; glutenin; starch; grain softness protein I; bacterial isoamylase; glycogen synthase; wSBE I-D4 gene; ss.
                                                                                                                        Claim 8; Page 75-81; 171pp; English.
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Ada72630 Rice gene
Ada72630 Rice gene
Ada72630 Rice gene
Ada73630 Full leng
Aaa467269 Pinus rad
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Aad472110 Rice gene
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A 1 40	wheat or barley. They can be used for the expression of e.g. wheat or barley. They can be used for the expression of e.g. se sequences of granule-bound synthase (GBSS), SBE II, low mol. tenin, grain softness protein I, bacterial isoamylase, bacteria n synthase, and wheat high mol. wt. glutenin BxI7. They can be r modifying the characteristics of starch produced by a plant. sequence represents the SBE II gene sequence. (Updated on 17-c standardise OS field) e 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other; e 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other; b 100.0%; Score 2050; DB 2; Length 11473; Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 1 CCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGTGTTGCCAAGAATTAAAAGGCTT 1 CGGAAGATAAATTCATATGCTAATTTTAGGGATGAGGTGTTGCCAAGAATTAAAAGGCTT 1 GGATACAATGCAGTGCAGATAATTGTAATTGTAGGAATCCAGGAGTGATGCAAGCTATTAGGG 2 CONTROLATGCAGTTCCAGATAATTGTTTAGGGATGCATCCATGTGGAAGCTATTACATGCG 2 CATTCACACAATCCAGTTCCAGTATATGTGTATACATCCTTCCACCCATTTTGGAGCTATTACATCC 2 TATTCACACAATCCATTTTTTTTTCTGTATACATCCTCTCCACCCATTTTGGAGCTATTACATCC 3 TATTCACACAATCCATTTTTTTCTGTATACATCCTCTCCACCCATTTTGGAGCTATTACATCC 3 TATTCACACAATCCATTTTTTTTCTGTATACACCCTCTTCCACCCATTTTGGAGCTATTACATCC 3 TATTCACACAATCCATTTTTTTTCTGTATACACCCCATTTTGGAGCTATTACATCC 3 TATTCACACAATCCATTTTTTTCTGTATACACCTCTTCCACCCATTTTGGAGCTATTACACTCC 3 TATTCACACAATCCATTTTTTTTTTTTTTTTTTTTTTT	8 8 8 8 8 8 8 8 8 8 8 8
44 00	CCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGTGTTGCCAAGAATTAAAAGGCTT	da da
4 4.	GGATACAATGCAGTGCAGATAATGGCAATTCAGGAGCATTCATACTATGCAAGCTTTACATCC TATTCAGACAATCCATTTTTTTTCTGTATACACTCTTCACCCATTTGGAGCTATTACATCC	Q dd S
Qy 18	1 TAA 8 TAA) b Q
n	1 ACACTTAG	g Q
· U	B ACACITAGIAITCIGAAAAAGATCAITITATIGITIGITIGGITICAGGAACAAGATCAIGTT 1 ACTAAITTTTTTGCACCAAGTAGCCGITTTGGAACTCCAGAGGACTTAAAATCCITGAIC 3	Db Qy
Qy 3:	CCHAGIAGCCGIIIIGGAACICCAGAGATATTGTTCATAGGTAATTAGTC 4	QY dd
Db 518 Qy 42	8 GAT	D Q
Db 52.	248 CAATTTAATTTTAGCTGTTTTACTGTTTATCTGGTATTCTAAAGGGAAATTCAGGCAATT 5307 481 ATGATACATTGTCAAAAGCTAAGAGTGGCGAAAGTGAAATGTCAAAATCTAGAGTGGCAT 540	уо
Db 53	308 ATGATACATTGTCAAAAGCTAAGAGTGGCGAAAGTGAAATGTCAAAATCTAGAGTGGCAT 5367	ر ور م
Qy 5.	541 AAGGAAAATTGGCAAAAACTAGAGTGGCAAAATAAAATTTTCCCATCCTAAATGGCAGG 600 	? B &
Qy 6	601 GCCCTATCGCCGAATATTTTTCCATTCTATATAATTGTGCTACGTGACTTCTTTTTTTCC 660	Db Q
Qy 66 Db 548	661 AGATGTATTAAACCAGTTGGACATGAAATGTATTTGGTACATGTAGTAACTGACAGTTC 720 	Q & &
Qy 7 Db 55	721 CATAGAATATCGTTTTGTAATGGCAACACTATTGATGCCATAGATGTGGATTGAGAACT 780 	\$ \$ \$
Qy 7	781 TCAGATGCTATCAATAGAATTAATCAACTGGCCATGTACTCGTGGCACTACATATAGTTT 840	0 b 4

ఠ	6748 TTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGATGCGGTAGTTTAC 6807	đ	4941 TATTCACACAATCCATTTTTTCTGTATACACNTCTTCACCCATTTGGAGCTATTACATC 5000
g Q	1981 TIGATGCIGGICAACGATCTAATTCATGGACTTTATCCTGATGCTGTATCCATTGGTGAA 2040 	g 4	180 CTAATGCTTCATGCACATAAAATATTTTGGATATAATCCTTTATTAGATATATAGTACAAC 239
g 9	2041 GATGTAAGTG 2050 6868 GATGTAAGTG 6877	עס מם	240 TACACTTAGTATTCTGAAAAAGATCATTTTATTGTTGTTGCTTGTTCCAGGTACCA 296
RESU		Qy db	297 TGTTACTAATTTTTTTGCACCAAGTAGCCGTTTTGGAACTCCAGAGGACTTAAAATCCTT 356
ig X F	AAH78338;	y 2	357 GATCGATAGAGCACATGAGCTTGGTTTGCTTCTTATGGATATTGTTCATAGGTAATT 416
ž Z	26-NOV-2001 (first entry)	0 V	AGTCCAATTTAATTTTAGCTGTTTTACTGTTTATCTGGTATTCTAAAGGGAAATTCAGGC
XBX	of a starch branching enzyme design	당 성	AGTCCAATTTAATTTTAGCTGTTTTACTGTTTATCTGGTATTCTAAAGGGAAATTCAGGC
\$ 2 2	Wheat; starch branching enzyme; BEIIb; SBE; transgenic plant; starch biosynthetic pathway; amylopectin; F2; amylose; ss.	γQ	
\$ 0 ×	Aegilops tauschii.	DЬ	5301 AATTATGATACATTGTCAAAAGCTAAGAGTGGCGAAAAGTGAAATGTCAAAATCTAGAGTG 5360
ž Z Z	WO200162934-A1.	γQ	537 GCATAAGGAAAATTGGCAAAAACTAGAGTGGCAAAAATAAAATTTTCCCATCCTAAATGG 596
\$ B \$	30-AUG-2001.	Дb	5361 GCATAAGGAAAATTGGCAAAAACTAGAGTGGCAAAAATAAAATTTTCCCATCCTAAATGG 5420
PRXF	21-FEB-2001; 2001WO-AU000175. 21-FEB-2000; 2000AU-00005742.	B 8	597 CAGGGCCCTATCGCCGAATATTTTTCCATTCTATATAATTGTGCTACGTGACTTCTTTTT 656
PA PA PA	(CSIR) COMMONWEALTH SCI & IND RES ORG. (GOOD-) GOODMAN FIELDER LTD. (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	Qy Db	657 TCTCAGATGTATTAAACCAGTTGGACATGAAATGTATTTGGTACATGTAGTAAGTGAACTGACA 716
2 E X	Morell M, Rahman S;	Qy	717 GTTCCATAGAATATCGTTTTGTAATGGCAACAACAATTTGATGCCATAGATGTGGATTGAG 776
\$ B \$	WPI; 2001-570635/64.	Db	5541 GTTCCATAGAATATCGTTTTGTAATGGCAACACAATTTGATGCCATAGATGTGGATTGAG 5600
YY Tra	Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat and barley.	g gy	777 AAGTTCAGATGCTATCAATAGAATTAATCAACTGGCCATGTACTCGTGGCACTACATATA 836
8888	Example 1; Fig 2; 103pp; English. The present sequence encodes a wheat starch branching enzyme of Aegilops	B 8	837 GTTTGCAAGTTGGAAAACTGACAGCAATACCTCACTGATAAGTGGCCAGGCCCCACTTGC 896
38888	genome donor of wheat. Probes isolated from the present sequence were used to identify type II starch branching enzymes (SBEs) in wheat, especially BEIIb. The BEIIb nucleic acids may be used to genetically	dd VQ	897 CAGCTTCATACTAGATGTTACTTCCCTGTTGAATTCATTTGAACATATTACTTAAAGTTC 956
38888	nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant	D Qy	957 TICATITGICCTAAGTCAAACTICTITAAGTITGACCAAGTCTATTGGAAAATATATCAA 1016
r m o	98.8%; Score 2025; DB 5; Length 11475; ilarity 99.8%; Pred. No. 0;	B 8	1017 CATCTACAACACCAAATTACTTTGATCAGCAGTTAACAATTTTATTTTATTATATTAGCAC 1076
N N	1 CCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGTGTTGCCAAGAATTAAAAGGCTT 60	g dy	1077 ATCTTTGATGTTGTAGATATCAGCACATTTTTCTATAGACTTGGTCAAATATAGAGAAGT 1136
γ _Q	61 GGATACAATGCAGATAATGCAATTCCAGGAGCATTCATACTATGCAAGCTTTGGG 120	B 5	1137 TTGACTTAGGACAAATCTAGAACTTCAATCAATTTGGATCAGAGGGAACATCAAATAATA 1196
₹ 8	4881 GĠÁTÁCAÁTGCAGTGCAGATAÁTGGCAATCCAGGAGCATTCATACTÁTGCAÁGCTTTTGGG 4940 121 TATTCACACAATCCATTTTTTTTTTTTTTTTTTTTTTT	Q	TAGATAGATGTCAACACTTCAACAAAAAAAATCAGACCTTGTCACCATATATGCATCAGAC
X	/ TATTEMERICALITITITE GIBLACACE TO LICENCE CALLINGUAGE LATERCATE 1/9		

RESUL AAZ35 AAC AC AC AC AC AC AC AC AC AC AC AC AC	25 A2 A3	4	00 00 00 00 00	5	70
LT 3 5393 AAZ35393 standard; DNA; 23449 BP. AAZ35393; 27-MAR-2000 (first entry) Maize amylose-extender (Ae) gene encoding starch branching enzyme. Starch branching enzyme IIb; amylose-extender gene; Ae gene; maize; corn; promoter; expression control element; endosperm; transgenic plant; ss. Zea mays.	1977 THACTIGATECTEGETCHANTICATEGETTTATCCTGATECTGATCCATTEGE 2000 6801 THACTIGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTATCCATTEGE 6860 2037 TGAAGATGTAAGTG 2050	621 TGTGCTACGGAGTCTTAGATAGTTACCTAGTATGCTTGTACAATTTTACCTGATGAGATC 668 857 ATGGAAGATTGGAAGTGATTATTATTTATTTTCTTTCTAAGTTTGTTT		261 ACACATTACTTCCACGAGAGTGGTCCACGGGGCATCATTGGATGTGGGATTCTCGTCTATTC 632 497 AACTATGGGAGGTGGGAAGTATGTAGGTAGCTCTGTTCTGTCACCATATTTGGGTAACTGTT 155 497 AACTATGGGAGGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGGGTAACTGTT 638 321 AACTATGGGAAGTTTGGAAAGTATGTAGCTCTGACACTATTTTGGCTAACTGTT 161 557 CCTGTTAATCTGTTCTTACACACATGTTGATATTCTATTCTATTGCAGGTATTGAGATTCTT 161 381 CCTGTTAATCTGTTCTTACACACATGTTGATAATTCTATTCTTATGCAGGTATTGAGATTCTT 644	GETTTAGCCACTTGCTTTCATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New gene regulatory sequences from plants used to provide resistance to microbial path pathogens.
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                                                                                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of the maize amylose-extender (Ae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 19; Page 98-105; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1999;
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12-JUN-1998;
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                                                                                                                                                                                                                                                                12623 TCTGGÁTGGGTTGAATGGTTTTGATGGTÁCAGATÁCACÁTTACTTTCACAGTGGTCCACG
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                                                                                                     1583 GATATICTATICTTAIGCAGGTATIGAGATICITACIGICAÀACGCGAGATGGIGGCTIG
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    ACGGATTACAAGTAATTTAAGCTTTATGCCTGTTAGTTTATCT-----TCACTTGCTA 1297
                     ATGGATTACAAGTAAGTCATCAAGTGGTTTCAGTAACTTTTTTTAGGGCACTGAAACAATT 1762
                                                     AGGAATATAAGTTTGATGGTTTCGGTTTTGATGGTGTGACCTCCATGATGTACACTCATC
                                                                     AAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGACCCTCCATGATGTATACTCACC
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98US-0089050P
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           Query Match 11.8
Best Local Similarity 63.1
Matches 463; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding wheat starch branching enzyme IIb, useful altering the amylose and amylopectin content of cereal plants, \boldsymbol{e}. and barley.
                                                                                                                                               The present sequence represents a partial genomic sequence of a wheat starch branching enzyme, designated BEIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-2001
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                         Claim 6; Page 95-98; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CSIR ) COMMONWEALTH SCI & IND RES
(GOOD-) GOODMAN FIELDER LTD.
(LIMA-) GRP LIMAGRAIN PACIFIC PTY I
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biosynthetic path
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                                                                                                     2134 A; 1788 C;
                                  11.8%;
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             Score 241.2; DB 5;
Pred. No. 9.6e-46;
0; Mismatches 223;
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                                                                                                     1829 G;
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                    Indels
                                                              8381;
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RESULT 5
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                                                                                                                                                                          Wheat;
starch
                                                                                                                                                                                                                                           Nucleotide sequence of wheat starch branching enzyme 9 (BEIIa)
                                                                                                                                                                                                                                                                                       26-NOV-2001
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  21-FEB-2001; 2001WO-AU000175
                                           30-AUG-2001
                                                                                     WO200162934-A1
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                                                                                                                                                                          starch branching enzyme; BEIIa;
biosynthetic pathway; amylopecti
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                                                                                                                                                                                                                                                         RESULT 6
AAX34650/c
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The present sequence encodes wheat starch branching enzyme 9, designated BEIIa. The specification describes BEIIb. BEIIb is a type II starch branching enzyme (SEE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the
       Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS; starch branching enzyme; starch soluble synthase; debranching enzyme; endosperm; wheat; barley; granule-bound synthase; glutenin; starch; grain softness protein I; bacterial isoamylase; glycogen synthase; wSBE I-D4 gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CSIR ) COMMONWEALTH SCI & IND RES OR (GOOD-) GOODMAN FIELDER LTD. (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD
                                                                                                                                                                                                                                         AAX34650 standard; DNA; 11473
                                                                                                                Starch branching enzyme II (SBE II) gene sequence.
                                                                                                                                                                                                      AAX34650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1228 TACTTCCACGGTGGTCCACGTGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT
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                                                                                                                                                                                                                                                                                                                             CTCCATGATGTATACTCACCATGGATTACAAATGA 1414
                                                                                                                                                                                                                                                                                                                                                 CTCCATGATGTATACTCACCATGGATTACAAGTAA 1717
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                                                                                                                                                  (revised)
(first entry)
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RESULT 7
AAH78338/c
ID AAH783

AAH78338

standard;

26-NOV-2001

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Query Match 6.2%;
Best Local Similarity 64.6%;
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 75-81; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated cereal plant enzyme genes used for, e.g. expression antisense sequences of granule bound synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-229525/19.
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(AUSU )
(GOOD-)
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20-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11473 BP; 3096 A; 2263 C; 2423 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morell M, Rahman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMONWEALTH SCI & IND
UNIV AUSTRALIAN NAT.
GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC I
                                                                                                                                                                                                                                                                                                                                                                  GTCAAACTTCTCTATATTTGACCAAGTCTATAGAAAAATGTGCTGATATCTACAACATCA
                                                                                                                                                                         AGATATCAGCACATTTTTCTATAGACTTGGTCAAATATAGAGAAGTTTGACTTAGGACAA
                                                                                                                                                                                                                                                                                                  AATTACTTTGATCAGATTAACAATTTTTATTTTATTATTAGCACATCTTTGATGTTGT
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                                                   ATCTAGAACTTCAATCAATTTGGATCAGAGGGAACATCAAATAATATAGAT 1201
                                                                                                                                                                                                                                         ÄÄGATGTGCTAATATÄATÄÄÄÄTAAAATTGTTAATCTGATCAAAGTAATTTGGTGTTGT
ATGAAGAACTTTAAGTAATATGTTCAAATGAATTCAACAGGGAAGTAACAT 5738
                                                                                                                  <u>AGATGTTGATATTTTTCCAATAGACTTGGTCAAACTTAAAGAAGTTTGACTTAGGACAA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97AU-00009108.
98AU-00002509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 126.2; DB 2;
Pred. No. 5.2e-19;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3691 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
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RESULT 8
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Best Local S
Matches 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a wheat starch branching enzyme of Aegilops tauschil, designated F2. A. tauschil is likely to be the ancestral D genome donor of wheat. Probes isolated from the present sequence were used to identify type II starch branching enzymes (SBEs) in wheat, especially BSIID. The BEIID nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to var levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheat;
starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CSIR )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2001; 2001WO-AU000175
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biosynthetic path
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                     GTCAAACTTCTTTAAGTTTGACCAAGTCTATTGGAAAATATATCAACATCTACAACACCA 1030
                                                                                                                                                                                                                                                                                                                                       AUGITACTICCCIGITGAATICATITGAACATATTACTTAAAGTTCTTCATTTGTCCTAA 970
                                                                                                                                  ATCTAGAACTTCAATCAATTTGGATCAGAGGGAACATCAAATAATATAGAT 1201
                                                                                                                                                                                         AGATATCAGCACATTTTTCTATAGAGATTTGGTCAAATATAGAGAAGTTTGACTTAGGACAA 1150
                                                                                                                                                                                                                                                    AATTACTTTGATCAGATTAACAATTTTTATTTTATTATTATTAGCACATCTTTGATGTTGT
                                                                                                                                                                                                                                                                                    GTCAAACTTCTCTATATTTGACCAAGTCTATAGAAAAATGTGCTGATATCTACAACATCA
                                                                                                                                                                                                                              <u>AAGATGTGCTAATATAATAAAATAAAATTGTTÄATCTGATCAAAGTAATTTGGTGTTGT</u>
                                                                                                                   ATGAAGAACTTTAAGTAATATGTTCAAATGAATTCAACAGGGAAGTAACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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                                                                                                                                                                                                                                                                                                                                                                                                           64.6%;
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Pred. No. 5.2e-19;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BEIIb; SBE; transgenic
ylopectin; F2; amylose;
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Rice
                                           DNA sequence
                                           Seq
                                           ID523
                                           related
                                           ő
                                           grain
                                           filling
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plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; gene; ds; plant.

Oryza sativa. 03-JAN-2003 WO2003000905-A2

22-JUN-2001; 2001US-0300112P. 26-SEP-2001; 2001US-0325277P. 20-DEC-2001; 2001US-0342327P. 21-JUN-2002; 2002WO-IB002450

(SYGN) SYNGENTA PARTICIPATIONS ĀG

Zhu T, Cheng W, Briggs S, Glazebrook J, Katagiri F, Cooper B, Goff SA, Kreps J, Provart N, Moughamer Ricke D;

2003-229341/22. DB; ADC08219.

New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved in the plant grain useful in generating nutritional properties.

Claim 35; SEQ ID NO 523; 130pp; English

This invention, in the area of plant biotechnology, relates to novel polymucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

Sequence 2304 BP; 610 A; 457 C; 620 G; 617 T; 0 U; 0 Other;

Similarity

91.5%;

2e-18; DB 9;

Length

2304;

Query Match Best Local Sim Matches 130; 1969 1354 1909 rtacaeereecartracteecaactateeceaaratriteeartrectactearctreat TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTTGCTACTGATGTTGAT GCCATTGGTGAAGATGTCAGCG TCCATTGGTGAAGATGTAAGTG Conservative o ;-Score 122.8; Pred. No. 2e-1 0; Mismatches 2050 12; Indels 0 Gaps 1473 2028 1413 1968 0

RESULT 9
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ID ADA7

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18-050-000 ADC08218; ADC08218

standard;

DNA;

2304

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ADA71289 standard; DNA;

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RESULT 10
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Matches 130; Conserv
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Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to patternal, fingal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID NO 4612; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.
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                                                                         AAV05639 standard; cDNA
                                                                                                                                                                                                                                                                                                                                                             Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;
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                                                AAV05639;
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                                                                                                                                            GCCATTGGTGAAGATGTCAGCG
                                                                                                                                                                                                                                                                                                                                                                                         the invention.
                                                                                                                                                                                                                                                                                                          Conservative
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91.5%;
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Pred. No. 2.1e-18;
0; Mismatches 12
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25-MAR-2003 01-MAY-1998

(revised) (first entry)

RESULT 11
ADC07807
ID ADC077
XX ADC07
X

ADC07807 standard; DNA; 2307

Rice DNA sequence Seq ID73 related to grain filling

(first entry)

plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn; comato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; gene: dg: plant

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Best Local Similarity
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                                                                                                                                                                  Sequence 3015 BP; 796 A; 606 C; 819 G;
                                                                                                                                                                                       The present sequence encodes the rice type IV starch branching enzyme, which has the ability to synthesise amylopectin. The quality of starch improved by the use of the protein. (Updated on 25-MAR-2003 to correct field.)
                                                                                                                                                                                                                                                                       Rice starch branching enzyme gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
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                                                                                                                                                                                                                                                                quality starch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
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                                                                                                                                                                                                                                         Claim 4; Page 5-8; 13pp; Japanese
                                                                                                                                                                                                                                                                                              P-PSDB; AAW41763.
                                                                                                                                                                                                                                                                                                                                                            24-JUN-1996;
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                                                                                 TTACAGGTGGCATTTACTGGCGAACTATGGCGAATATTTTGGATTTGGATGTTGAT
                                                                                                      TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT
GCCATTGGTGAAGATGTCAGCG
                                        GCAGTAGTTTACTTGATGCTGGTGAACGATCTAATTCATGGGCTTTATCCTGAGGCTGTA
                                                           GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA
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                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               starch branching enzyme; amylopectin synthesis;
                                                                                                                                                                                                                                                                                                                             GYOSAI SHOKUBUTSU TOATSU CHEM INC.
                                                                                                                                                                                                                                                                                                                                                             96JP-00162983
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288. .2651
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129. .287
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
129. .2654
                                                                                                                        6.0%; Score 122.8; DB 2;
91.5%; Pred. No. 2.2e-18;
Live 0; Mismatches 12;
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1767
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Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention, in the area of plant biotechnology, relates to novel polynucleotides comparising a mucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, cannola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhu T, Cheng W, Briggs
Glazebrook J, Katagiri 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-2002; 2002WO-IB002450
Starch branching enzyme IIb; SBEIIb; corn; maize; antisense; amylopectin;
                              Corn starch
                                                              10-SEP-1997
                                                                                              AAT69737
                                                                                                                              AAT69737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                          1895
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)B; ADC07808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; SEQ ID NO 73; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                    ATCCTGATGCTGTATCCATTGGTGAAGATGTAAGTG 2050
                                                                                                                                                                                                                                                                                             CTACTGATGTTGATGCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTT
                                                                                                                                                                                                                                                                                                                                                                    AAGTTTGTTTCTTGTTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTG
                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                           ATGTATACTCATCATGGTTTACAGCATTTACTGGCAACTATGGCGAATATTTTGGATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2307 BP; 608 A; 465 C; 620 G; 614 T; 0 U;
                                                                                                                                                                                                              ATCCTGAGGCTGTAGCCATTGGTGAAGATGTCAGCG 1434
                                                                                                                                                                                                                                                                           CTACTGATGTTGATGCAGTAGTTTACTTGATGCTGGAGCGATCTAATTCATGGGCTTT
                            branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                              (first entry)
                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                     85.88
38;
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Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                      Score 119.2;
Pred. No. 1.4e
0; Mismatches
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                              IIb gene fragment in pBE96
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, Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                                       1.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2307;
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Ricke D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 Other;
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                                                                                                                                                                                                                                                                                                             2014
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AAT69736;
ID AAT69736;
XX AAT69736;
AC AAT69736;
XX DE COIN Starch brack
XX St
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Best Local S
Matches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A cDNA insert (AAT69737) in plasmid pBE96 comprises a 2.09 kb fragment of corn starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729), starting at the initiating ATG codon of the coding region and terminating 312 bp 5' of the translation termination codon. It was obtd. by site-specific mutagenesis of the SBEIIb gene in plasmid pBE240 to generate an NcoI site at the ATG start site, and EcoRI digestion of the mutagenised plasmid. The 2.09 kb fragment was inserted, in sense orientation, between the zein promoter and 3' regions in vector pML103 to produce pBE96. Cosuppression and antisense techniques can be used to inhibit SBEIIb in transgenic plants and thereby alter starch properties
                                                                                                                                                                                                  Starch branching enzyme IIb; transgenic plant; pBE45; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2087 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopecuseful in preparation of thickened foodstuff.
                                                                                                                                                                                                                                                                                          Corn starch branching enzyme IIb gene fragment in pBE45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 56-57; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                    10-SEP-1997
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131; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTCATGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACAT 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGAACTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACTTTCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTAT 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACTTCCACGGTGGTCCACGGGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Pred. No. 1.3e-15;
                                                                                                                                                                                                                                       SBEIIb;
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                                                                                                                                                                                                                                          corn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                          amylopectin;
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WO9722703-A2

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RESULT 14
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KW Starco
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Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A 2.16 kb cDNA insert (AAT69736) in plasmid pBE45 comprises the entire 5' untranslated region as well as 2.08 kb of the coding region of corn starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729). It was generated by EcoRI digestion of plasmid pBE240 and was inserted into vector pMLD103 in antisense orientation with respect to a maize 27 kba zein promoter and a 10 kba zein gene 3' sequence. Transgenic corn plants expressing the near full-length SBEIIb antisense transcript demonstrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff.
                                                                                                                                                                                                                    Non-glycogen-like polysaccharide production; fermentation; starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis; non-starch branching gene; amylopectin; amylose; plant-like starch; maize branching enzyme II; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2165 BP; 593 A; 580 C; 416 G; 576 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                            DNA encoding
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                                                                        04-APR-1997;
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                                                                                                    03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unique starch branching phenotype
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             Keeling PL
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                                            GENETICS LLC
                                                                         97US-0042939P.
                                                                                                     98WO-US006660.
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                                                                                                                                                                                                                                                                                            branching enzyme II.
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79.4%;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and non-food applications of these starches are useful for all food and non-food applications of starch. The present sequence is used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing non-glycogen-like polysaccharides in bacteria, fungi or platransformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2640 BP; 715 A; 510 C; 686 G; 729 T; 0 U; 0 Other;
                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                    AAT69729 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 53; 150pp;
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                                                                                                                                                                                                                                                                                       Starch branching etransgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                        AAT69729;
                                                                                                                                                                                                                                                                                                                                Plasmid pBE240 insert encoding corn
                                                                                                                                                                                                                                                                                                                                                             10-SEP-1997
                                                                                            20-DEC-1995;
                                                                                                                        12-DEC-1996;
                                                                                                                                                   26-JUN-1997
                                                                                                                                                                            WO9722703-A2
                                                                                                                                                                                                                                                               Zea mays.
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DB; AAW70895.
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                                                                                              95US-0009113P
                                                                                                                         96WO-US019678
                                                                                                                                                                                                                     Location/Qualifiers 79. .2478
                                                                                                                                                                                                                                                                                       enzyme IIb; ; pBE240; ss.
                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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Pred. No. 1.4e-15;
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                                                                                                                                                                                                                                                                                                       SBEIIb; corn;
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WPI; 1997-341694/31. P-PSDB; AAW19212.

Hubbard NL,

Klein TM,

Broglie KE

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Search completed: April 10, 2004, 04:00:06 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2665 BP; 700 A; 525 C; 705 G; 735 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A CDNA insert (AAT69729) in plasmid clone pBE240 comprises a 2.7 kb EcoRI -XhoI fragment isolated from a corn cDNA library. It includes an open reading frame encoding starch branching enzyme IIb (SBEIIb) (AAM19212). The insert was used as a starting point in the assembly of DNA constructs (see also AAT69730, AAT69736-37) designed to achieve suppression of SBEIIb expression in transgenic corn plants, and thereby to produce novel starches that have properties beneficial in food and industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 50-53; 92pp; English.
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Perfect score:
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6. /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Listing first 45 summaries
    Copyright
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(c) 1993 - 2004
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US-09-731-166-9
US-09-257-894-8
US-09-257-894-8
US-09-257-894-11
US-09-9131-166-11
US-09-087-277-1
US-09-658-499-1
US-09-658-499-1
US-09-257-894-25
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Patent No. 6570066

GENERAL INFORMATION:
APPLICANT: Willinitzer, et al.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT
TITLE APPLICATION NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES SEQ
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US-09-609-040-3
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Best Local Simi
Matches 244;
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ORGANISM: Triticum a
FEATURE:
NAME/KBY: CDS
LOCATION: (313)..(24
OTHER INFORMATION: E
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44; Conservative
                                 AAACGCGAGATGGTGGCTTGAAGAATATAAGTTTGATGGÄTTTTCGATTTGATGGGGTGAC
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US-08-165-315D-3
US-08-165-315D-3
US-09-105-390-13
US-09-105-390-5
US-09-633-326-2
US-09-633-326-2
US-09-633-326-2
US-09-631-976-2813
US-09-621-976-2813
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Pred. No. 1.9e-28;
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Patent No. 6639126
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccarides
FILE REFERENCE: 35718/206348
                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
SEQ ID NO 9
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Best Local :
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CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (0)...(0)
OTHER INFORMATION: SBEIIa
OTHER INFORMATION: Genbank Accession No. 5639126 U55948
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ORGANISM: Zea mays
FEATURE:
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LOCATION: (2)...(2446)
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APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC comparible
OPERATING SYSTEM: Microsoft Windows 95
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                                                                                                                                 STREET: 100/ Fun-
CITY: Wilmington
                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACTTCCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502
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                                                                                                                           Delaware
                                                                                                                                                                    E. I. du Pont de Nemours and Company
1007 Market Street
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88.1%;
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Pred. No. 1.2e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOROLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 131;
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APPLICATION NUMBER: 09/091,05
PILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el St
TITLE OF INVENTION: Enzyme Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Form Compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Version 7.0A CURRENT APPLICATION DATA:
        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                    CITY: Wilmington
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                                                                     CLASSIFICATION:
                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                           COUNTRY:
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5. 6376749
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                                                                                                                                                                                                                                                                                               Delaware
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79.4%;
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Pred. No. 1.4e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Hubbard, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: MO. 6376749el Starches via Modification
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Bryme Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELECHONE: 302-992-4926
TELEPHONE: 302-992-4926
TELEPHONE: 302-973-0164
                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1007 Mar
CITY: Wilmington
                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Delaware
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                                                                                                                                                                                                                                                                 US/09/257,894
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; LOCATION: (101)...(2500)
US-09-731-166-11
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; Sequence 11, Application US/09731166
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                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FAST
SEQ ID NO 11
LENGTH: 2720
                                                                                                                                                                              Query Match 5.4%;
Best Local Similarity 79.4%;
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.4%;
Best Local Similarity 79.4%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccarides
FILE REPERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6639126
                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Genbank Accession No. 6639126 AF072725
                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
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LENGTH: 2665 base pa
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STRANDEDNESS: sing
     1503
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                                                                          1443
                                                                                                                                  1383 AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
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                                                             TACTICCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502
                                                                                                             AGTCATGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACAT 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version
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                                       TACTTTCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTAT
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     GGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGG
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Pred. No. 1.6e-19;
0; Mismatches 34
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                                                                                                                                                                              Score 110.6; DB 4
Pred. No. 1.6e-19;
0; Mismatches 34
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                                                                                                                                                                                  34; Indels
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       1547
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GGGAACTGGGAAGTTTTAAGATTTCTTCTCCCAATGCTAGATGG

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RESULT 7
US-08-941-445A-14
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                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (303) 499-808
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 50
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: not TOPOLOGY: mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/026,855 FILING DATE: 30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2725 base pairs
                                                                                        1443
                                                                                                                       1228
1348
                                                                                                                                             1383 AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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6107060
                                                                                                                                                                                               Similarity
                         GGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGG 1547
                                                                                  TACTTCCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT
                                                                                                                       AGTCATGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACAT 1287
GGGAACTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGG 1392
                                                           TACTTTCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTAT 1347
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                                                                                                                                                                                  Conservative
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265..2487
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                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                               5.48;
79.48;
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                                                                                                                                                                                               Score 110.6; DB 3
Pred. No. 1.6e-19;
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                              Length 2725;
                                                                                                                                                                                  Indels
                                                                                                                                                                                 0;
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RESULT 9 US-09-658-499-3

Sequence 3,

Application US/09658499

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: EX, BO
APPLICANT: KHOSNOOI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: LARSSON, Hakan
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER APPLICATION NUMBER: SE 9504272-7
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Matches
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                                                                                                                                                                                                                                                                                                                                         Query Match
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NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown FEATURE:
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:bell gene fragment OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser,
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (422)...(424)
OTHER_INFORMATION: Amino acid 141 is Xaa wherein Xaa =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n
OTHER INFORMATION: C, G or T.
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                                                                                                                                                                                                                                                                                         Local Similarity 78.9
nes 112; Conservative
                                                                                                                                                                                                                                    1909 TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTTGGATTTTGCTACTGATGTTGAT
                                             2029 TCCATTGGTGAAGATGTAAGTG 2050
                                                                                             794
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o. 6169226
                                                                                                                                   GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
                                                                                           GCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTTCCCCAGATGCAATT
ACCATTGGTGAAGATGTTAGCG
                                                                                                                                                                                                                                                                                                             4.6%;
78.9%;
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Pred. No. 2.9e-15;
0; Mismatches 30
875
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INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
SEQ ID NO 3
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US-09-087-277-1
                                                                             Sequence 1, Application US/09087277B Patent No. 6169226 GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: STARCH BRANCHING ENZYME
FILE REFERENCE: 003300-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EK, BO
APPLICANT: KHOSNOODI,
APPLICANT: LARSSON, C
APPLICANT: LARSSON, H
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1393
TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Nucleotides 424, OTHER INFORMATION: C, G or T. NAME/KEY: misc feature LOCATION: (422)...424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Unknown Organism:bell gene fragment OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1148)..(1150)
OTHER INFORMATION: Amino acid 383 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (2)..(1393)
NAME/KEY: misc_feature
LOCATION: (424)...(1150)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                             ACCATTGGTGAAGATGTTAGCG 875
                                                                                                                                                                                                                                                            TCCATTGGTGAAGATGTAAGTG
                                                                                                                                                                                                                                                                                                         GCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCCAGATGCAATT 853
                                                                                                                                                                                                                                                                                                                                    GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA
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LARSSON, Hakan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 94; DB .
Pred. No. 2.9e.
0; Mismatches
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ches 30;
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TCCATTGGTGAAGATGTAAGTG

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APPLICANT: RASK, LATS
TITLE OF INVENTION: STARCH BRANCHING ENZYME II
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1996-11-29
EARLIER FILING DATE: 1995-11-29
EARLIER FILING DATE: 1995-11-29
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                             US-09-087-277-1
                                                                                                                                                   Matches 112;
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                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430,
OTHER INFORMATION: n wherein n = A, C, G or T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                           PEANTURE:
NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFOEMATION: Amino acid 608 is Xaa wherein
                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (1896)...(1898)
OTHER INFORMATION: Amino a
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: sig_peptide
LOCATION: (189)..(332)
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LOCATION: (189)..(2825)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Unknown OTHER INFORMATION: (branching enzyme II) i OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa =
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid
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LOCATION: (1404)..(140
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                                                                                                           1909 TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT
                                                                                                                                                                     Similarity
GCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCCAGATGCAATT 1859
                           GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA
                                                                         TTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGAT
                                                                                                                                                 Conservative
                                                                                                                                                                     4.6%;
78.9%;
                                                                                                                                                                                                                                                                                                                                               acid
                                                                                                                                                   Score 94; DB
Pred. No. 4.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                             522
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                                                                                                                                                                     4.2e-1
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1860 ACCATTGGTGAAGATGTTAGCG 1881

Patent No. 64692 GENERAL INFORMAT

1, Application
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US/09658499

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                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid 5:
OTHER INFORMATION: or Phe.
NAME/KEY: misc feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 6:
15-09-658-499-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver.
SEQ ID NO 1
                                                                                                                 Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: STARCH BRANCHING ENZYME FILE REFERENCE: 00300-486 CURRENT APPLICATION NUMBER: US/09/658,499 CURRENT FILING DATE: 2000-09-08 PRIOR APPLICATION NUMBER: 09/087,277 PRIOR FILING DATE: 1998-05-29 PRIOR APPLICATION NUMBER: PCT/SE96/01558 PRIOR FILING DATE: 1996-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EK, BO
APPLICANT: KHOSNOODI
APPLICANT: LARSSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1996-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LARSSON, HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 100
OTHER INFORMATION: n wherein n = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (189)..(2825)
NAME/KEY: sig_peptide
LOCATION: (189)..(332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Unknown Organism:beII gene OTHER INFORMATION: (branching enzyme II) from Solanum tubero: OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1404)...(1406)
OTHER INFORMATION: Amino acid
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Amino acid -16 OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (285)..(287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 3074
1969 GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
                                                                                                               Similarity 78.1
12; Conservative
                                                           TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTTGGATTTGCTACTGATGTTGAT 1968
                                     TTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGAT
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LARSSON, Clas-Tomas
                                                                                                                               4.6%;
78.9%;
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58
                                                                                                               Score 94; DB 4;
Pred. No. 4.2e-15;
0; Mismatches 30
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NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 647621:

NAME/KEY: unsure
LOCATION: 245, 254, 265, 281, 294

OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6200
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RESULT 13
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CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SOFTWARE: DNA
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                            Matches 123;
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYMUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays
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                                                                                                                                                                              1635 GTGGCTTGAAGAATATAAGTTTGATGGATTTCGATTGATGGGGTGACCTCCATGATGTA 1694
                                                                                               1695 TACTCACCATGGATTACAAGTAAGTCATCAAGTGGTTTCAGTAACTTTTTTAG 1747
                                                                                                                                                                                                                                                                   1575 CACATGITGATATTCTATTCTTATGCAGGTATTGAGATTCTTACTGTCAAACGCGAGATG
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                                                                                                                                              GTGGCTCGAGGAATATAAGTTTGATGGTTTTCCGTTTTGATGGTGTGACCTCCATGATGTA
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                                                                  CACTCACCACGGATTACAAGTAACATTTACGGGGAATTCAATGAGTATTTNGG 247
                                                                                                                                                                                                                             CGCCTATTTAAACTATGGGAACTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lalgudi, Raghunath V.
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                               4.68;
71.18;
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Pred. No. 1.9e
0; Mismatches
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1.9e-15;
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US-09-330-330-3
Sequence 3, Application US/09330330
Patent No. 6274789
GENERAL INFORMATION:
APPLICANT: Yano, Masahiro
APPLICANT: IMamoto, Masao
APPLICANT: Katayose, Yuichi
APPLICANT: Katayose, Yuichi
APPLICANT: Wang, Zi-Xuan
APPLICANT: Yamanouchi, Utako
APPLICANT: Yamanouchi, Utako
APPLICANT: Ishimaru, Lisa
TITLE OF INVENTION: RICE GENE RESISTANT
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
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BLAST DISEASE

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Sequence 25, Application US/09257894 Patent No. 6376749
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10322 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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COMPUTER: ISM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
PROTICATION NUMBER: US/09/330,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Ph.D., J.D., Janis K. REGISTRATION NUMBER: 34,819
REGERENCE/DOCKET NUMBER: 06501/032001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1:
FILING DATE: 12-JUN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: Microsoft Windows SOFTWARE: Version 7.0A CURRENT APPLICATION DATA:
                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10322 base pairs
TYPE: nucleic acid
STRANGENESS: single
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                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  961 TTTGTCCTAAGTCAAACTTCTTTAAGTTTGACCAAGTCTATTGGAAAATATATCAACATC 1020
                                                                                                                                                                                                                                                                            Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAACACGAAATTAGTTTCATTAAATGTAGCATTGAATATATTTTGATAGTATGTTTGT 5116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTTTCCAGTCAAACTTCTTT-AGTTTGACCAAGTTTATACAAAATTTAGCAACATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTTAGGACAAATCTAGAACTTCAATCAATTTGGATCAGAGGGAACAT 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGTGTTGAAAATGCTGCTATATTTTTTAAAAAAACTTGGTCAAACCTAAACAAGTTTG 5176
                                                                                                                                                                                                                                             Delaware
                                                                                                                                                                                                                                                                                                     E. I. du Pont de Nemours and Company
1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATGTTGTAGATATCAGCACATTTTTCTATAGACTTGGTCAAATATAGAGAAGTTTG 1139
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Wlein, Theodore M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hubbard, Natalie L
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63.6%;
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Pred. No. 1.2e-09;
0; Mismatches 81
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Best Local Similarity
Matches 97; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1. PAGE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0:
FILING DATE: JUNE 10, 19:
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                SOFTWARE: Version 7.0A CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 6376749e.
TITLE OF INVENTION: Expression of TITLE OF INVENTION: Enzyme Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
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                                                                                                                                                                                     APPLICATION NUMBER: US/09/257,894 FILING DATE:
      NAME: Majarian, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   955 GGCACACCAGAGGACCTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTTGCGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 GGAACTCCAGAGGACTTAAAATCCTTGATCGATAGAGCACATGAGCTTTGGTTTGCTTGTT
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1007 Market Street
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Klein, Theodore M.
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linear
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No. 6376749el Starches via Modification
Expression of Starch Biosynthesis
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Pred. No. 3.7e-09;
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RESULT 14 US-09-257-894-25

COUNTRY:

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Page 8
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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10621.793 Million cell updates/sec
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12 US-10-434-893A-3

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15 US-10-260-238-1027

12 US-10-260-238-253

15 US-10-260-238-2253

15 US-10-260-238-2253

15 US-10-260-238-2253

15 US-10-260-238-2253

16 US-10-260-238-2253

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Sequence 3, Appli
Sequence 1, Appli
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Sequence 1027, Ap
Sequence 253, Appli
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US-10-434-893A-3

Sequence 3, Application US/10434893A

Publication No. US20940060083A1

Publication No. US20940060083A1

Publication No. US20940060083A1

APPLICANT: Ahmed Regina

APPLICANT: Matthew Kennedy Morell

APPLICANT: Sadequr Rahman

TITLE OF INVENTION: Containing products with an increased amylose content

FILE OF INVENTION: Containing products with an increased amylose content

FILE REFERENCE: 69425

CURRENT ETLING DATE: 2003-05-09

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 2.1

SOFTWARE: Patentin version 2.1

FYPE: DNA

OPERATION: Application US/10/434,893A

CURRENT ETLING DATE: 2003-05-09

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 2.1
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; OTHER INFORMATION: SSBEIIa gene
US-10-434-893A-3
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                                                                                                                                           Query Match 98.8%; Score 2025; I Best Local Similarity 99.8%; Pred. No. 0; Matches 2049; Conservative 0; Mismatches
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FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(11476)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4820 CCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGTGTTGCCAAGAATTAAAAGGCTT
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         61 GGATACAATGCAGTGCAGATAATGGCAATCCAGGAGCATTCATACTATGCAAGCTTTTGGG
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4 US-10-254-534-1
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19 US-09-938-842A-337
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12 US-10-415-058-14
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Result No.

1017 CATCTAGAACACCAAATTACTTTGATCAGATTAACAATTTTTATTATTATTAAGAC 1076	O CAGCTTCATACTAGATGTTACTTCCCTGTTGAATTCATTTGAACATATTACTTAAAGTT 7 TTCATTTGTCCTAAGTCAAACTTCTTTAAGTTTGACCAAGTCTATTGGAAAATATATAT	CTGGC	ATAGAATATCGTTTTGTAATGGCAACACAATTTGATGCCATAGATGTGGATTGAG 77	CAGGGCCCTATCGCCGAATATTTTCCATTCTATATAATTGTGCTACGTGACTTCTTTT 54 CAGGGCCCTATCGCCGAATATTTTTCCATTCTATATAATTGTGCTACGTGACTTCTTTT 54 TCTCAGATGTATTAAACCAGTTGGACATGAAATGTATTTGGTACATGTAGTAAACTGACA 71	537 GCATAAGGAAAATTGGCAAAAACTAGAGTGGCAAAAATAAAATTTTCCCATCCTAAATGG 596 [CAGGC 52 CAGGC 53 CAGTG 53	7 GATCGATAGAGCACATGAGCTTGGTTTGCTTGTTCTTATGGATATTGTTCATAGGTAATT 416 1	240 TACACTTAGRATICTGAAAAGAICATTITATTGTTGTTGTTGCCAGGTACCA 296	O CTAATGCTTCATGCACATAAAATATTTGGATATAATCCTTTATTAGATATATAGTACAAC 2	121 TATTCACACAATCCATTTTTTTCTGTATACAC-TCTTCACCCATTTGGAGCTATTACATC 179 19
RESULT 2 US-10-434-893A-1 US-10-434-893A-1 , Sequence 1, Application US/10434893A , Publication No. US20040060083A1 , Publication No. US20040060083A1 , GENERAL INFORMATION: APPLICANT: Ahmed Regina APPLICANT: Matthew Kennedy Morell APPLICANT: Sadequr Rahman TITLE OF INVENTION: Barley with altered branching enzyme activity and starch TITLE OF INVENTION: containing products with an increased amylose content FILE REFERENCE: 69425 CURRENT APPLICATION NUMBER: US/10/434,893A	Db 6800 TTACTTGATGCTGATCCTAATTCATGACTTTATCCTGATGCTGTATCCATTGG 6859 QY 2037 TGAAGATGTAAGTG 2050 Db 6860 TGAAGATGTAAGTG 6873	1917 GACATTTACTGGGAACTATGGCGAATATTTTGGATTTTGCTACTGATGTTGATGCGGTAGT 1	67 91 73	6500 GGTG 1737 AACT 6560 AACT	QY 1617 ACTGTCAAACGCGAGATGGTGGCTTGAAGAATATAAGTTTGATGGATTTCGATTTGATGG 1676	Db 6320 AACTATEGGAAGTIAGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGGCTAACTGTT 6379 QY 1557 CCTGTTAATCTGTTCTTACACATGTTGATATTCTTATGCAGGTATTGAGATTCTT 1616	Qy 1437 ACACATTACTICCACGGTGGTCCACGGGCCATCATTGGATGTGGGATTCTCGTCTATTC 1496	Db 6140 CTTCTACTTGGTTTGGTTTGATTCTATTTCAGTTGCATTGCTTCATCAATGATTTTGTGTA 6199 Qy 1377 CCCTGCAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGAT 1436 Db 6200 CCCTGCAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGAT 6259	Qy 1257 CATCTGTITGCTTTAGCCACTTGCTTTCATATTTATGTGTTTTGTACCTAATCTACTTTTC 1316 Db 6080 CATCTGTTTGCTTTAGCCACTTGCTTTCATATTTATGTGTTTGTACCTAATCTACTTTTC 6139 Qy 1317 CTTCTACTTGGTTTGGTTGATTCTATTTCAGATTGCATTGCTTCAATCTACTTTTTGTGTA, 1376	

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CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO 1
LENGTH: 2554
TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
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US-10-434-893A-3/c
; Sequence 3, Application US/10434893A
; Publication No. US20040060083A1
; GENERAL INFORMATION:
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                                                                                                                             ; OTHER INFORMATION: SSBEIIa gene US-10-434-893A-3
                                                                                                                                                                                                                                                                                  APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadegur Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 3
LENGTH: 11476
LENGTH: 11476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.8%; Score 139.4; DB 12; Best Local Similarity 71.9%; Pred. No. 9.3e-22; Matches 241; Conservative 0; Mismatches 6;
                                                       Query Match 6.2%;
Best Local Similarity 64.6%;
Matches 188; Conservative
                                                                                                                                                            TYPE: DNA
ORGANISM: Aegilops tauschii
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(11476)
OTHER INFORMATION: n is a, c,
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1101
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911 ATGTTACTTCCCTGTTGAATTCATTTGAACATATTACTTAAAGTTCTTCATTTGTCCTAA
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                                                       Score 126.2; DB 12; Length Pred. No. 2.4e-18; O; Mismatches 103; Indels
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                                                                                          Length
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   RESULT 5
US-10-434-893A-4
; Sequence 4, Application US/10434893A
; Publication No. US20040060083A1
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APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1027
LENGTH: 1442
TYPE: DNA
                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Oryza sativa
US-10-260-238-1027
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US-10-260-238-1027
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Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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443
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                       ATTCAACTATGGGAGTTGGGAAGTATGTAGCTCT 1526
                                                                                                           TGATACACATTACTTCCACGGGGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCT
                                                                                                                                                            TGTTCACAGCAGCCATGCGTCAAATAATACCCTAGATGGGTTGAACGGTTTGATGGTAC
                                                                                                                                                                                              TGTACCCTGCAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCAC
TTTCAACTATGGGAATTGGGAAGTTCTAAGATTT 476
                                                                               AGATACGCATTACTTTCATAGTGGTTCACGCGGCCATCATTGGATGTGGGATTCTCGCCT
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Goff, Stephen A.
Katagiri, Fumiyaki
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Provart, Nicholas
Ricke, Darrell
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Indels

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Gaps

876 999

936

1178 996 Length 2000;

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TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
LENGTH: 2000
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CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
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APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadegur Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
TITLE OF INVENTION: containing products with an increased amylose content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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NAME/KEY: MISC FEATURE
LOCATION: (1)...(6550)
OTHER INFORMATION: n is a, c, g or t
FEATURE:
OTHER INFORMATION: partial SSBEIIb gene
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glazebrook, Jane
Goff, Stephen A.
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Ricke, Darrell
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Pred. No. 3.1e-15;
0; Mismatches 48
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; TYPE: DNA
; PEATURE:
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2443)
; OTHER INFORMATION: SBEII modified region
US-10-397-954A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pearlstein, Richard W.
APPLICANT: Broglie, Karen E.
APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Eleptic Reference: BB1510 US A.
CURRENT APPLICATION NUMBER: US/10/397,954A
CURRENT EILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR FILING DATE: 2002-03-27
PRIOR PILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-05-16
NUMBER: MISCOCFT WEST. MISCOCFT MISC. MISCOCFT MISC
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; ORGANISM: Oryza
US-10-260-238-2253
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 172;
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Best Local
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                                                                                                                                                                                                                                                                                                                                  1909 TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTTGGATTTGCTACTGATGTTGAT 1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 CATATTACTTAAAGTTCTTCATTTGTCCTAAGTCAAACTTCTTTAAGTTTGACCAAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
                                                                                                                                                                                                                                                                              TTACAAGTAACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGAT 1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAGGAAAATGTAGCAGCATCTACAACACCAAATTAGTTTATTAAATGTAACATTGAATA
                                                                                               TCCATTGGTGAAGATGTAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGAACATCAAATAAT 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCAAACTTTAAAAAGTTTGACAAAGGAAAAAGTCAAAGCGACTTATAATATGAAATGG 1056
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                                       ACCATTGGTGAAGATGTTAGTG
                                                                                                                                                         GCAGTGGTTTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                        5.1%;
                                                                                                                                                                                                                                                                                                                                                                                      Score 105.2; DB 1
Pred. No. 7.8e-14;
0; Mismatches 23
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Pred. No. 3.9e-15;
                                       1170
                                                                                               2050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
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Gaps

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1148

Length 2443;

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APPLICANT: Allen, Steve
APPLICANT: Beckles, Diane M.
APPLICANT: Beckles, Diane M.
APPLICANT: Butler, Karla
APPLICANT: Pearlstein, Rich
TITLE OF INVENTION: Starch Branching Enzyme IIb
FILER REFERENCE: BB1439 US NA
CURRENT APPLICATION NUMBER: US/09/792,127
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/186098
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Office 97
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US-09-792-127-3
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                                                                                                                                                                                     ; LENGTH: 3039
; TYPE: DNA
; ORGANIZM: Triticum aestivum
US-09-792-127-3
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; ORGANISM: Triticum aestivum
US-09-792-127-1
                                                                                                                                                                                                                                                SOFTWALL.
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ballen, Steve
APPLICANT: Beckles, Diane M.
APPLICANT: Butler, Karla
APPLICANT: Butler, Karla
APPLICANT: Pearlstein, Rich
TITLE OF INVENTION: Starch Branching Enzyme IIb
FILE REFERENCE: BB1439 US NA
CURRENT APPLICATION NUMBER: US/09/792,127
CURRENT APPLICATION DATE: 2001-02-23
CURRENT FILING DATE: 2001-02-23
CURRENT FILING DATE: 2001-02-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                          Best Local Similarity 82.8 Matches 120; Conservative
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                                                                                                                                         Query Match
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PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 5
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Local Similarity 82.8%;
hes 120; Conservative
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1307 CAGTCACGCGTCAAATAATACCTTGGACGGGTTGAATGGTTTTGATGGCACGGATACACA 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1442 TTACTTCCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTA 1501
                                            1382 CAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACA 1441
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                                                                                                                                                                                                                                                                                                         Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTACTTCCATGGCGGTTCACGGGCCATCACTGGATGTGGGATTCCCGTGTGTTTAACTA 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGAATAAGGÁÁGTTATAÁGGTTT 971
                                                                                                                 5.1%;
82.8%;
                                                                                        Score 105; DB 9; Length 3039; 
Pred. No. 9.7e-14; 
0; Mismatches 25; Indels
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Pred. No. 8.8e-14;
0; Mismatches 25
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US-10-434-893A-2
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Publication No. US20040060083A1

GENERAL INFORMATION:

APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morel1
APPLICANT: Sadequr Rahman

TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and ITITLE OF INVENTION: containing products with an increased amylose content FILIS REFERENCE: 69425

CURRENT APPLICATION UNMBER: US/10/434,893A

CURRENT FILING DATE: 2003-05-09

NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 2.1
SEQ ID NO 2
LENGTH: 2780
TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
                                                                                                                                                                                                                                                                                               Query Match 5.0%; Score 101.8; DB 12; Length 2780; Best Local Similarity 77.0%; Pred. No. 5.1e-13; Matches 124; Conservative 0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: SSBEIID CDNA
1235 GTCACGCATCAAGTAATACCTTGGACGGTTTGAATGGTTTT 1275
                                                                                                                                                  350 AATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGTTCTTATGGATATTGTTCATA 409
                                                                                                                                                                                                                                                   290 GGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTTTGGAACTCCAGAGGACTTAA 349
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                                                                                                   GGTACCATGTTACCAATTTCTTTGCACCAAGTAGCCGTTTTGGGTCCCCCAGAAGATTTAA 1174
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                                            GGTAATTAGTCCAATTTAATTTTAGCTGTTTTACTGTTTAT 450
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US-10-260-238-2253/c
US-10-260-238-2253/c
Sequence 2253, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Moughamer, Todd G.
APPLICANT: Goff, Steven P.
APPLICANT: Goff, Steven P.
APPLICANT: Goff, Steven A.
APPLICANT: Katagiri, Funiyaki
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Ricke, Darrel1
APPLICANT: Ricke, Darrel1
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 6011-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
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; TYPE: DNA; ORGANISM: Oryza sativa US-10-260-238-2253
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                                                                                                               NAME/KEY: CDS
LOCATION: 145..2790
SEQUENCE DESCRIPTION: SEQ
US-10-056-454A-14
                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UNMBER: US/10/056,454A
FILING DATE: 25-Unn-2002
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/10056454A

Publication No. US20030166919A1

GENERAL INFORMATION:

APPLICANT: National Starch and Chemical Investment Holding Corporation

TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition

NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 2253
LENGTH: 2000
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 165;
                                       Matches 129;
                                                                          Query Match
                                                          Local Similarity
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ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1050 CATATTATAAGTCGCTTTGACTTTTTCCTTTGTCAAACTTTTTTAAAGTTTTGACCAAGTT
1865 TTGGAAGTGATTATTTATTTTCTTTCTAAGTTTGTTTCTTGTTCTAGATGACATTTA 1924
                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               999 ТАТТССАЛАЛАТАТАТСАЛСАТСТАСЛАСАССАЛАТТАСТТТСАТСАСАТТАЛСАТТТТ 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTTATTATTAGCACATCTTTGATGTTGTAGATATCAGCACATTTTTCTATAGACTT 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 19720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Delaware
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                                                                                                                                                                                                           TOPOLOGY:
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                                       Conservative
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                                                        4.6%;
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                                     Score 94.8; DB 14
Pred. No. 2.2e-11;
D; Mismatches 57
                                                                                                                                   ID NO: 14:
                                                                          DB 14;
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                                                                          Length 3033;
                                         Indels
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FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/10/254,534
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US/09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: US/09/087,277
PRIOR FILING DATE: 1996-05-29
PRIOR APPLICATION NUMBER: SCT/SE96/01558
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1996-11-29
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR TILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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US-10-254-534-3
; NAME/KBY: misc feature
; COATION: (1148)..(1150)
; OTHER INFORMATION: Amino
US-10-254-534-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10254534
Publication No. US20030046730A1
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APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Unknown Organism:bell gene fragment OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                      NAME/KEY: misc_feature
LOCATION: (890)..(89)
OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (422)...(424)
OCHER INFORMATION: Amino
                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
OTHER INFORMATION: C, G or T.
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LOCATION: (2)..(1393)
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LARSSON, Clas-Tomas
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Query Match Best Local Similarity

4.6%;

Score 94; Pred. No.

DB 14; 2.3e-11;

Length 1393;

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; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-2424
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                                                                                                                                                                                                                                                                                                                                        Query Match 4.6%;
Best Local Similarity 62.0%;
Matches 165; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                         CAGGTTATAAGATGTTTTAACTTTAGTCGAAGTCAAACTTTTTCAAGTTTGACTAAGTTT
GGGAACATCAAATATATAGATAGAT 1205
                                          ATCAAACTTAAAGCAGTTTGGCTTTGATCAAAGTCAAAACGTCTTAAAACCTGAAACGGA
                                                                                                                TTTTATTATATTAGCACATCTTTGATGTTGTAGATATCAGCACATTTTTCTATAGACTTG
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Ricke, Darrell
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iri, Fumiyaki
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GGGAGTACATTATTTTGAATTATAT 776

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RESULT 15
US-10-056-454A-16
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Search completed: April 10, Job time: 729.03 secs
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Best Local Similarity 78.9%;
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CORRESPONDENCE ADDRESS:
ADDRESSE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          1591
                                                                                                                                                                                                                          1969 GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA
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                                                                                                                                    2029 TCCATTGGTGAAGATGTAAGTG 2050
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                                                                                          ACCATTGGTGAAGATGTTAGCG 1612
                                                                                                                                                                                                                                                                        TTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Newcastle
STATE: Delaware
                                                                                                                                                                                  GCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCCAGATGCAATT 1590
                           2004, 20:07:35
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Maximum DB
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Perfect score:
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                                                                                                                Description
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Zea mays
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CC362748
                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 930)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
                                                                                                                                                             Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHLB23TB
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                                                                                                                                     Contact: Cathy Whitelaw
                                                                                                                                                                                                                                 Bennetzen, J.
                                                                                           Medical Center Drive,
                                                                      301-838-5843
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BQ245037 TB215032A
BU98666 HF12102r
AQ57666 nbxb0089J
CD890409 G118.114J
AV939010 AV939010
BU970967 HB16D15r
CA292638 SCRLFLB02
CA202517 SCRFFL102
AY109521 Zea mays
BM660711 952041B07
CA188652 SCCEPAM200
CA083722 SCEPAM200
CA083722 SCEPAM200
BA348549 hb58f11.9
BC04440703 WHE42022
BU0966891 HB02K24r
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AGG18655 OND58D100449
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AQ65765 AV165766
BZ667903 PUBBM33TD
BZ667903 PUBBM33TD
BZ348549 hb58f11.9
CA191146 SCCCRT12.0
AQ840558 nbxb00064F
CC992767 ZUAEN43TV
CD484414 EL01N043
CD43855 SC09b11 mem
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CG882826 985 bp DNA linear G
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ZMMBBb042B17 5', genomic survey sequence.
CG882826
CG882826 GI:38613949
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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/strain="B73"
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                                           GTTCATAGGTA 360
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Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C. Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c) Unpublished (2003)
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Zea mays subsp. mays (maize)

Zea mays subsp. mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bharti@waksman.rutgers.
Seq primer: T7
Class: BAC ends
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Tel: 732 445 3801
Fax: 732 445 5735
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The Plant Genome Initiative
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                                            GACCTAAAATATAATAGATAAAGCGCATGAGCTTGGCTTGCTAGTGCTTATGGATATT
                                                                                    GACTTAAAATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGTTCTTATGGATATT
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GTTCATAGGTA 413
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/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="ZMMBBb0492B17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sub_species="mays"
/db_xref="taxon:4578"
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/cultivar="B73"
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Matches 241; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-JUL-2002) to the EMBL/GenBank/DDBJ databases. Barker G., Institute of Arable Crop Research, Long Ashton, Bristol BS41 9AF United Kingdom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson I., Beswick R., Shepherd S., Barker G., Parker J., CEdwards D., Coghill J., Holdsworth M., Lenton J., Shewry P. "A BBSRC-funded wheat EST resource for the academic communi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum (mercia) clone E03_e411_plate_3 maternal tissue (minus endosperm and embryo) 6 days post anthesis
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                                                       AAACGCGAGATGGTGGCTTGAAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGAC 1682
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   CTCCATGATGTATACTCACCATGGATTACAAGTAA 1717
                                                                                                                                      AATCTGTTCTTACACATGTTGATATTCTATTCTTATGCAGGTATTGAGATTCTTACTGTC 1622
                                  AAACGCGAGATGGTGGCTTGAAGAATATAAGTTTGATGGATTTCGATTGATGGGGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="6 days post anthesis"
/tissue_type="maternal tissue (minus endosperm
/clone_lib="e:411"
/clone="E03_e411_plate_3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/cultivar="mercia"
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'moT_type="mRNA"
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72, Last updated, Version
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 476)
Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Barley ESTs from developing seeds
Unpublished (2002)
Contact: Stein Nils
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Tel: 039482-5522
Fax: 039482-5595
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Institute of Plant Genetics and Crop Plant
Corrensstr. 3, 06466, Gatersleben, Germany
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BU972445.1
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HB21K16r BC Hordeum vulgare subsp. vulgare
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Insert Length: 476 Std Error:
Plate: 21 row: X column: 16
Seg primer: Milrey.
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      AATCTGTTCTTACACATGTTGATATTCTATTCTTATGCAGGTATTGAGATTCTTACTGTC
                                                                                                                                                                                                            AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
                                                                                   GGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGGCTAACTGTTCCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="developing caryopsis"
/dev_stage="8-15 DAP (days after pollination)"
/lab_host="XL10-Gold"
/clone_lib="BC"
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/cultivar="barke"
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/db_xref="GABI:237282"
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Pred. No. 1e-16;
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                                                                                                                                                                                                                                                                  Indels 88;
                                                                                                                                                                                                                                                                                                Length 476;
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Best Local Similarity
Matches 241; Conserv
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                                                                              29
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Contact: Stein Nils
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Institute of Plant Genetics and Crop Plant Research (IPK)
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Striptophyta; Embryophyta; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 537)

1 (bases 1 to 537)
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HB03P08r BC Hordeum vulgare i 5-PRIME, mRNA sequence.
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Barley ESTs from developing seeds
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: stein@ipk-gatersleben.de
Insert Length: 537 Std Error:
Plate: 3 row: P column: 8
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TACTTCCACGGTGGTCCACGGGGCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502
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                                                                           AGTCATTCGTCAAATAATACCCCTTGACGGTTTGAATGGTTTTCGATGGCACTGATACACAT
                                                                                                    AGTCATTCGTCAAATAACCCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
                                                                                                                                                              6.8%; ilarity 71.9%; Conservative
                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); Site_2: XhoI (3'-end of CDNA); developing caryopsis, 8-15 DAP(days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PSII). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="developing caryopsis"
/dev_stage="8-15 DAP (days after pollination)"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sub_species="vulgare"
/db_xref="GABI:232152"
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/cultivar="barke"
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/mol_type="mRNA"
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1. .537
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/clone="HB03P08"
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                                                                                                                                                                Score 139.4; DB
Pred. No. 1e-16;
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Best Local S
Matches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wheat functional genomics - Glenlea developing seeds cDNA libr.

Unpublished (2002)

Contact: Dr. Sylvie Cloutier

Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9

Tel: (204) 983-2340

Fax: (204) 983-2340

Email: scloutier@aggr.gc.ca
was cloned directionally, not all sequences generated with reviperimer were from the 5' end (same with forward primer and 3' end primer were size is 3-1.4 kb

Plate: 032 row: A column: 02

Seq primer: M13 Reverse.

Seq primer: M13 Reverse.
      202 GCGGTCGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ245037

476 bp mRNA linear EST 03-MAY-2002
TaE15032A02R TaE15 Triticum aestivum cDNA clone TaE15032A02R, mKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum (bread wheat)
Triticum aestivum
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                                                                                                                                                                                               Similarity
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                                                                                       TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT 1968
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                             GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGĞACTTTATCCTGATGCTGTA 2028
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                                                                                                                                                                       6.5%;
ilarity 96.5%;
Conservative
                                                                                                                                                                                                                                                                                /clone="TaE15032A02R"
/clone="TaE15032A02R"
/tyssue_type="developing seeds"
/dev_stage="15_days_after_anthesis"
/lab_host="E. coli_DH10B"
/clone_lib="TaB15"
/clone_lib="TaB15"
/note="TaB15"
/note="TaB15"
/site_1: NotI; Site_2: MluI; mRNA obtained from wheat see of cultivar Glenlea 15 days post-anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Glenlea"
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Pred. No. 1.1e-15;
0; Mismatches 5;
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EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 623)
Radchuk, V, Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Barley ESTs from developing seeds
Unpublished (2002)
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HF12IO2r HF Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
BU986646
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
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Insert Length: 623 Std Error: 0.00
Plate: 12 row: I column: 2
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     GGGAGTTGGGAAGTATGTAGCT 1524
                                                                                   TACTTCCACGGTGGTCCACGGGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502
                                                         TACTTCCACGGTGGTCCACGTGGCCATCATTGGATGTGGGATTCTCGTCTGTTCAACTAT 582
                                                                                                                                                                                                                                                                          6.5%; Score 134; DB 13; Length 623; ilarity 96.5%; Pred. No. 1.1e-15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="HF"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Geveloping caryopsis, 16-25 DAF(days after flowing) Due to a cloning caryopsis, 16-25 DAF(days after flowing) Due to a cloning cartefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.Average insert size is 940 bp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
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/dev_stage="developing caryopsis, 16-25 DAF (days after
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/clone="HF12I02"
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/db_xref="GABI:246586"
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                                                                                                                                                                         Query Match
Best Local Similarity
Matches 344; Conserv
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        1529 CTTCTGTCACCATATTTGGCTAACTGTTCCTGTTAATCTGTTCTTACACATGTTGATATT 1588
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 610)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ576669 610 bp DNA linear GSS 02-
nbxb0089J01r CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nbxb0089J01r, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
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                                                                                                    GTGGGATTCTCGTCTATTCAACTATGGGAGTTGGGAAGTA------TGTAGCTCTGA 1528
                                                               GTGGGATTCTCGCCTTTTCAACTATGGGAATTGGAAGTAAAGGAACACGTTAATCGCTCT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                 / clone "nbxb008901"

/(tissue_type="Leaf"
//tissue_type="Leaf"
//tissue_type="Leaf"
//lab host="3. coli DH10B"
//clone_lib="CUGI Rice BAC Library"
//clone_lib-"CUGI Rice BAC Library"
//clone_lib-"CUGI Rice BAC Library"
//clone_lib-"CUGI Rice BAC Library"
//clone_library for the world population especially those
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledomous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library contains 36,864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
                                                                                                                                                                      6.5%; Score 133.2; DB 28; Length 610; llarity 59.1%; Pred. No. 1.5e-15; Conservative 0; Mismatches 168; Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
|mol_type="genomic DNA"
|strain="Japonica"
|cultivar="Nipponbare"
|db_xref="taxon:39947"
                                                                                                                                                                                 70;
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REFERENCE
AUTHORS
TITLE
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SOURCE
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                                                                                                                                  93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
CD890409
CD890409.1 GI:32659746
                                                                                                                                                                                                                                                                      Genoplante, a major partnership Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD890409 621 bp
G118.114J06F010718 G118 Triticum
                                                                                                                                                                                                                                                        Contact: Genoplante
                                                                                                                                                                                                                                                                                                     Genoplante.
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1 (bases 1 to 621)
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                 /tissue_type="grain
pollination)"
                                                                        /mol_type="mRNA"
/cultivar="recital"
                                              /clone="G118114J06"
                                                            'db_xref="taxon:4565"
                                                                                                        organism="Triticum aestivum'
clone_lib="G118"
                                  (118
                                                                                                                                                                                                                                                                                     french
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TITLE
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DEFINITION
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ATTGTTCATAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTT
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al Similarity
136; Conserv
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1 (bases 1 to 678)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato,K., Saisho,D. and Takeda,K. Barley EST sequencing project in Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV939010
AV939010.1 GI:18234807
                                                                                                                                                                                                                                    Similarity
                                                                          GAGGACTTAAAATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGTTCTTATGGAT
                                                                                                                                 GCGAGCTTTGGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTTTGGAACTCCA
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ATTGTTCATAGGGTAATTAGTCCAATTTAATTTTAGCTGTTTTACTGTTT
                                                                                                                                                         GCTTGTTCCAGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTTTTGGAACTCCA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   /tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone lib="K. Sato unpublished cDNA library,
adult, heading stage top three leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                 sub_species="spontaneum"
db_xref="taxon:77009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'mol_type="mRNA"
'strain="H602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Hordeum vulgare subsp. spontaneum"
                                                                                                                                                                                                                                                                                                                                                                                                         lone="bah20e24"
                                                                                                                                                                                                                                    6.1%;
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0; Mismatches
                                                                                                                                                                                                                Score 125.8; DB 9
Pred. No. 3.9e-14;
D; Mismatches 27
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Best Local Sim
Matches 131;
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618 bp mRNA
SCRLFL8025G06.g FL8 Saccharum officinarum
5., mRNA sequence.
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Doales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Hordeum.
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Insert Length: 411 Std Error: 0.00
Plate: 16 row: D column: 15
Seq primer: Ml3rev.
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Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
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Radchuk, V., Zhang, H., Weschke, W.,
Barley ESTs from developing seeds
Unpublished (2002)
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HB16D15r BC Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
BU970967
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                                                                                                                                                                                                                                                                                                                                                GCGGTGGTTTACTTAATGCTGGTCAACGATCTAATTCATGGACTTTATCCGGATGCTGTA 263
                                                                                                                                                                                                                                                                                                                                                                            GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
                                                                                                                                                                                                                           rccarreereaacarercaece 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 124.4; DB 13; Length 411; ilarity 92.3%; Pred. No. 8.1e-14; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hordeum vulgare subsp. vulgare"
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/clone="HB16D15"
/tissue_type="developing caryopsis"
/tissue_type="developing caryopsis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SX+; Site_1: EcoRI (5'-end of CDNA); Site_2: KhoI (3'-end of CDNA); developing caryopsis, 8-15 DAP(days after pollination) Due to a cloning arrefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BambI, SalI,PBtI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
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                                           EST 26-SEP-2003
e SCRLFL8025G06
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                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                              338
                                                                                                                             SCRFFL127B04.9 FL1
5', mRNA sequence.
CA202517
CA202517.1 GI:3523
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enkaryota; Viridiplantae; Iilionaida: Poales: Poacese: PACCAD
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                                                                                                                                                                                                                              bp mRNA
m officinarum
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Query Match 6.0%; Score 123.2; DB 14; Length 618; Best Local Similarity 91.0%; Fred. No. 1.3e-13; Matches 131; Conservative 0; Mismatches 13; Indels 0;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.

El (bases 1 to 618)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

RS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact; Arruda P
Contact; Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas
Tal: 55 19 3788 1137
Fax: 55 19 3788 1137
Fax: 55 19 3788 1039
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
plate: 025 row: G column: 06
Seq primer: T7 Promoter Primer.

S column: T1 Promoter Primer.
                                                                                                          1443 TACTTCCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGGTCTATTCAACTAT 1502
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Saccharum officinarum"
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/db_xref="taxon:4547"
/clone="SCRLFIB025G06"
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/clone=lib="FL8"
/note="Organ: Developing inflorescence and rachis
/note="Organ: Developing inflorescence and rachis
/note="Organ: Developing inflorescence and rachis
/note="Organ: Developing inflorescence and rachis (10cm-long)]. CDNA was prepared
inflorescence and rachis (10cm-long)]. CDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.io.unicamp.br/public"
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Clone distribution: clone distribution information cathrough the Brazilian Clone Collection Center (BCCC)
http://www.boccenter.fcav.unesp.br
plate: 027 row: B column: 04
Seq primer: T7 Promoter Primer.
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Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
                                                                                                                                                                                Zea mays
Zea mays
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Tea mays CL1245_1 mRNA sequence.
AY109521
AY109521.1 GI:21213273
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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clade; Panicoideae; Andropogoneae; Saccharum.
                                        Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                       Overgo Probes
                                      Maize Mapping Project/DuPont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
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                                                                                                 (bases 1 to 2766)
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Pred. No. 1.2e-13;
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BM660711
LOCUS
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Matches 133
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Zea mays
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Submitted (25-APR-2002) Maize Mapping Project, University of Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.rmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nin.gov. When the source of tww.tigr.org; or NCBI, www.ncbi.nlm.nin.gov. When the source of the columbia columbia and the columbia columbia. Stanford or Pat maize CDNA sequences is either Virginia Walbert, Stanford or Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (base Coe, E.H.
                                                                                                                                                          Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Email: walbot@stanford.edu
Plate: 952041 row: B column:
Cocation/Qualifiers
1...399
                                                                                     855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                            Unpublished (1999)
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BM660711
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/mol_type="mRNA"
/db_xref="MaizeDB:630161"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
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0; Mismatches 18
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ssue from Walbot Lab (reduced rRNA)
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Search completed: April 10, 2004, 14:06:33 
Job time : 5423.32 secs
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/clone lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
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/mol type="maNS (Black Mexican Sweet)"

/db_xref="taxon:4577"

/db_xref="taxon:4577"

/tissue_type="suspension culture"

/dev_stage="mixed logarithmic and stationary growth
phases"
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18: em ov:*

21: em ov:*

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22: em ov:*

23: em pat:*

24: em pht:*

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27: em sto:*

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Pred. No.

is the number of results predicted by chance to have

REFERENCE AUTHORS TITLE

Li,Z., Morell,M. and Rahman,S. Regulation of gene expression in plants

RESULT 1
AXO31271
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
KEYWORDS
SOURCE
ORGANISM

11463 bp Sequence 10 from Patent WO9914314. AX031271 AX031271.1 GI:10278603

DNA

linear

PAT 20-SEP-2000

ALIGNMENTS

Aegilops tauschii Aegilops tauschii Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Eurmatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Aegilops. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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GCTATTTCTTAATCAGGTGGCCTTGGACTCTGACGATGCACTCTTTGGTGGATTCAGCAG
                                                                                                                                    CTCAGTTGGACTCGGTCTAATACTAGAACTATTTTCCGAATCTACCCTAACCATCCTAGC 720
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                                                                                AGTTTTAGAGCAGCCCCATTTGGACAATTGGCTGGGTTTTTGTTAGTTGTGACAGTTTCT
                                                                                                                 CTCAGTTGGACTCGGTCTAATACTAGAACTATTTTCCGAATCTACCCTAACCATCCTAGC
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N FIELDER LTD (AU); LI ZHONGYI (AU); MORELL MATTHEW (AU);
SADEQUR (AU); UNIV AUSTRALIAN (AU); COMMW SCIENT IND RES
U); GROUPE LIMAGRAIN PACIFIC PTY L (AU)
                                                  TAGAGCAGCCCCATTTGGACAATTGGCTGGGTTTTTGTTAGTTGTGACAGTTTCT
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Rahman,S., Regina,A., Li,Z., Sh
Direct Submission
Submitted (18-JAN-2001) Plant I
Canberra, ACT 2601, Australia
Location/Qualifiers
                                                                                                                                                                                                                                             Aegilops tauschii
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Aegilops.

1 (bases 1 to 11475)
Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M.,
Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
starch-branching enzyme IIa from the wheat genome donor Aegilops
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Aegilops tauschii starch
AF338431 GI:13447949
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 ATTTGTAAAGAAATTTGCTCGAGCTGTTGTAGCCATAGGAAGGTTGTTCTTAACAG
                                                   TTTAATTCCACATGGATAGAGTTTGTTGGTCGTGCAGCTATCAATATAAAGAATAGGGTA
                                                                                                                     TATGCTTGCCTTTCATTGTCCACCCTTCACCAGTAGGGTTAGTGGGGGCTTCTACAACT
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CRRRFDLGDADPIRTYRGMGFFDDAVGVLFETHHDDDAVFTTEHPHDN
RPRSFSVYTPSRTAVVYALTE"
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/product="starch branching enzyme IIa"
/poin(1204. .136,1664. .1761,2038. .2279,2681. .2779,2949. .2991,3144. .3203,3539. .3219,3703. .3819,4105. .4818. .4939,5115. .5234,6209. .6338,6427. .6537,6739. .7447. .7550,8392. .8536,9556. .9703,9839. .9939,10116. .10395. .10550,10928. .111092. .11175)
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Sequence 10
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AX756279.1
Zhu,T., Cheng,W., Briggs,S., Cooper,B., Golf,S.A., Glazebrook,J., Katagiri,F., Kreps,J., Provart,N. ar Identification and characterization of plant genes Patent: WO 03000905-A 1018 03-JAN-2003;
                                                                                              Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                  Pooideae;
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Sequence
AR340173
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1 (bases 1 to 2853)

1 (limitzer, L., Kroger, C., Lutticke, S. and Lorz, H. Willmitzer, L., Kroger, C., Lutticke, S. and Lorz, H. Nucleotide sequences encoding enzymes that alter the concentration and composition in plants patent: US 6570066-A 3 27-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-AUG-1996) University of Hamburg, Institute of General Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr. 18, Hamburg 22609, Germany Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 2853)
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U66376
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Query Match Best Local

Similarity

27.5%; 100.0%;

Score 370; Pred. No.

DB 8;

Length 2853;

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McCue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D.

Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum cv. Cheyenne): Molecular Characterization, Developm Expression, and Homolog Assignment by Diffferential PCR Plant Mol. Biol. Rep. 20 (2), 191-192 (2002)

2 (bases 1 to 2970)

McCue, K.F. and Anderson, O.D.

Direct Submission

Submitted (11-JUL-2000) United States Department of Agricult Submitted (11-JUL-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum
Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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94710-1105, USA
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SWKMGDIVHTITNRRWLEKCVTYASSHDQALVGDKTIAFWLMDKDMYD-MALDREGTP
RIDGGIALHKMIRLVTWGLGGESYLLWMGNEFGHPSWIDFPGGVCTPTGKVLPGNNN
SYDKGRRFDLGDADFLRYHGMQEFDDAMQHLEEKYGFMTSEHQYVSRKHEEDKVIIF
ENGILVFVRBHWSNSFDYRYGCSRFGKYKVALDSDDALFGGFSRLDHDVDYFTTEH
ENGILVFVRBHWSNSFDYRYGCSRFGKYKVALDSDDALFGGFSRLDHDVDYFTTEH
PHDNRPRSFSVYTPSRTAVVYALTE"
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961 GAACATCCGCATGACAACAGGCCGGGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
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                                                            CTGAACCCTCCTACTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG 1320
                                                                                                                                                                             CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGGAGCAGATGGATAG 1200
                                                                                                                                                                                                                                                                                         CCCGTGCGCTCAACGTGAAAAT 1342
                               CT--ACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                               GTAGCTTGTTGGTGAGCGCTCGAAAGAAAATGGACGGGCCTGGGTGTTTGTCGTGCTGCA
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Pred. No. 7.9e-91;
0; Mismatches 4
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tauschii
Plant Physiol.
21140316
                                                                Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M.,
Kosar-Hashemi,B., Abrahams,S. and Morell,M.C.
Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
relationships among isoforms the wheat genome donor Aegilops
                                                                                                                                                                                                                                                                                             Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum
                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Pooideae, Triticeae, Triticum.
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IIa variant mRNA,
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KEYWORDS
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Y11282.1 GI:1885343
1,4-alpha-glucan bra
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T.aestivum mRNA for starch branching
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KFSVQAPGEIPFNGIYYDPPEEXYVPQHQPKREELHITSHSHIGMSSPEPKINSYA
NFRDEVLPRIKRLGYNAVQIMAIQEHSYASFGYHVTNNFFAPSSFFTPEDLKSLIDR
AHELGILVLNDIVHSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHMWDSRLFNYGSWE
VLRFILSNARWHLEXYKFDGFREDGVISMMYTHHGLQWTFTGNYGEYFGFATDVDAVV
YLMIVNDLIHGLHPDAVSIGETREDGVISMMYTHHGLQWTFTGNYAEYFGFATDVDAVV
YLMIVNDLIHGLHPDAVSIGETREDGVISMMYTHHGLQWTFTGNYDFWALDRP
STERIDRGIALHKWIRLVTMGLGGEGYLNFMGNEFGHPWIDFPRGPQTLFTGKYLPG
NNNSYDKCRRFPDLGDADFLRYHGMQEFDQAMQHLEEKYGFMTSEHQYVSRKHEEDKV
IIFERGDLYFVTNHKNNSFFDYRVGGSRFGKYKVALDSDDALFGGFSRLDHDVDXFT
TEHPHDNRPRSFSVYTPSRTAVVYALTE"
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/mol_type="mRNA"
/db_xref="taxon:4565"
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 branching
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 enzyme; sbe2 gene; starch branching
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375; Conserv
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961 GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGGTGTACACTCCGAGCAGAACTGCG 1020
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Triticum aestivum (bread wheat)
Triticum aestivum
Viridiplantae; Strep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, CANADA
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Chibbar, R.N.
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GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db xxef="G1.10313"
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2930. .2935
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2948
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2879. .2884
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151. .2622
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313. .2619
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                                                                                                                                                Score 360; DB 8;
Pred. No. 2.2e-90;
0; Mismatches 5
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	CDS	gene		JOURNAL FEATURES source	REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS		SOURCE ORGANISM	VERSION KEYWORDS	DEFINITION	RESULT 9 AF064560		0у 1321	Qy 1261 Db 2839	Qy 1201 Db 2779	Qy 1141 Db 2719	QY 1081 Db 2659	Qy 1021 Db 2599
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Source Source ORIGIN Ouery Match Best Local Simil Matches 169; C		TITLE Direct JOURNAL Submit	Sperma Sperma Sperma Pooide REFERENCE 1 (based on Tingey Caraba	SOURCE TRIBLE SOURCE TRIBLE ORGANISM TRIBLE ENkary	Z	RESULT 10 BT008928 LOCUS DEFINITION Trition	Db 2485 TGTA	1300	2428	1244	Qy 1201 GTAG	Db 2308 CGCC	2248	OY 1081 CTCC	Qy 1021 GTCG	Qy 961 GAAC Db 2128 GAAC	Query Match Best Local Simil Matches 343; C	ORIGIN	

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VALDSDDALFGGFSRLDHDVDYFTTBHPHDNRPRSFSVYTPSRTAVVYALTE"
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ct Submission
fited (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and itted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and any, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
                                                                                                                                                                                                                                                                                                                      icum aestivum (bread wheat)
icum aestivum
yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
deae; Triticeae; Triticum.
bases 1 to 2549)
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larity 90.9%; Pred. No. 2.3e-33;
Conservative 0; Mismatches 17;
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larity 87.5%;
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                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:32128479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays subsp. mays (maize)

Zea mays subsp. mays

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoldaee; Andropogoneae; Zea.
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Zea mays subsp. mays cultivar CML333 amylose extender
starch-branching enzyme (ael) gene, exons 19 through 22 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA Location/Qualifiers
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Whitt, S.R., Wilson, I.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clack, Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1373 bp DNA linear PLN 20-APR-200:
Zea mays subsp. mays cultivar A6 amylose extender starch-branching
enzyme (ae1) gene, exons 19 through 22 and partial cds.
AY235395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1373)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1373)
Whitt,S.R., Wilson,L.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTATTTTGACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTATGCATCTATC 519
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/number=22
                                                   /translation="GDADYLRYHGMQEFDQAMQHLEQKYEFMTSDHQYISRKHEEDKVIVFEKGDLVFVFNFHCNNSYFDYRIGCRXPGVVKVVLDSDAGLFGGFSRIHHAAEHFT
  /gene="ael"
/number=19
                                                                                                                                                                                           join(<57. .134,401. .556,1010. .1084,1181.
/gene="ae1"</pre>
                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays subsp.
/mol_type="genomic DNA"
/cultivar="A6"
                                                                                                                 Coodon start=1
(product="amylose extender starch-branching enzyme")
protein id="AAP05849.1"
db_xref="GI:30026535"
                                                                                                                                                                                                                 product="amylose extender starch-branching enzyme" | oin (<57. .134,401. .556,1010. .1084,1181. .1264)
                                                                                                                                                                                                                                                    |Oin(<57. .134,401. .556,1010. .1084,1181. .>1373)
|gene="med"
                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4578"
                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.9%; Score 132.4; DB 8
83.0%; Pred. No. 6.3e-26;
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AY235421
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Best Local
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Zea mays subsp. mays
Ewaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1374)
Whitt,S.R.; Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                            Submitted (12-FEB-2003) Genetics, USDA-ARS, North University, 3513 Gardner Hall, Box 7614, Raleigh, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY235421 1374 bp DNA linear PLN 20-P
Zea mays subsp. mays cultivar TX601 amylose extender
starch-branching enzyme (ael) gene, exons 19 through 22 and
                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                        Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and
                                                                                                                                                                                                                                                                                                                                                                                               22247734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTAACTGCAGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATA
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/gene="ae1"
/number=22
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/gene="ae1"
/number=20
1010. .1084
/gene="ae1"
/number=21
 join(<58. .135,402. .557,1011. .1085,1182. .>1374)
/gene="ael"
/product='amylose extender starch-branching enzyme
join(<58. .135,402. .557,1011. .1085,1182. .1265)
/gene="ael"
/codon start=1
                                                                                                                                                 /organism="Zea mays subsp. mays"
/mol type="genomic DNA"
/cultivar="TX601"
/db xref="taxon:4578"
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Pred. No. 6.3e-26;
0; Mismatches 31;
extender starch-branching enzyme"
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NC 27695, USA
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AY235405
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JOURNAL
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Best Local Similarity 83.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571 TT 572
                                                                                                            Direct Submission
Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
                                                                                                                                                                                                                                                                                                                           Zea mays subsp. mays (maize)
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Zea.
                                                                                                                                                                                                                                                                 I (bases 1 to 1382)

Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY235405 Inear PLN 20-APR-2003 Zea mays subsp. mays cultivar D940Y amylose extender starch-branching enzyme (ael) gene, exons 19 through 22 and partial
                                                                                                                                                                                             2 (bases 1 to 1382) Whitt,S.R., Wilson,L.M.,
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1011. .1085
/gene="ae1"
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cultivar="D940Y"
       /db_xref="taxon:4578"
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/db_xref="GI:30026587"
                                                                                                     Location/Qualifiers
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>1382
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Pred. No. 6.3e-26;
0; Mismatches 31;
                                                                                                                                                                                              Tenaillon, M.I.,
                                                                                                                                                                                                Gaut, B.S.
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                                                                    PUBMED
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                                                                                                       Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002) 22247734
                                                                                                                                                                                        Zea mays subsp. mays (maize)
Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                  AY235396 Inear PLN 20-F
Zea mays subsp. mays cultivar B103 amylose extender
starch-branching enzyme (ae1) gene, exons 19 through 22 and
                                                                                                                                                                                                                                                                                                 AY235396
AY235396.1
Direct Submission
Submitted (12-FEB-2003)
                                                 2 (bases 1 to 1393)
Whitt, S.R., Wilson, L.M.,
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/gene="ae1"
/number=22
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/number=21
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1011. .1085
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Ivfekgdlvfvfnfhcnnsyfdyrigcrkpgvykvvldsdaglfggfsrihhaaehft
adcshdnrfysfsvytpsrtcvvyafve"
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join(<57. .134,402. .557,1011. .1085,1182. .>1382)
/gene="ae1"
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/protein_id="AAP05859.1"
/db_xref="GI:30026555"
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oin(<57. .134,402. .557,1011. .1085,1182. .1265)
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Pred. No. 6.3e-26;
0; Mismatches 31;
   Genetics,
                                                       Tenaillon, M.I.,
   USDA-ARS,
                                                       Gaut, B.S.
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   Carolina
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ilarity 83.0%;
Conservative
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1176. .>1393
/gene="ae1"
/number=22
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/number=20
1005. 1079
/gene="ael"
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Ivfekgdlvfvfnfhcwnsyfdyrigcrkfgvykvvldsdaglfggfsrihhaaehft
adcshdwrpysfsvytfsrtcvvyafve"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Zea mays subsp.
/mol_type="genomic DNA"
/cultivar="B103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="amylose extender starch-branching enzyme"
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/product="ammylose extender starch-branching enzyme"
/oin(<57. .134,401. .556,1005. .1079,1176. .1259)
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                10,
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Pred. No. 6.3e-26;
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Title:
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
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DB seq length: 2000000000
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10857.595 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	iption
ь ¦	4	100.0	11473	2 !	AAX34650	Aax34650 Starch br
N	1344	00.		ហ	7833	Aah78338 Nucleotid
ω	37	27.	1119	φ	3871	н
4	67.	.7	979	ω	994	2 Nucleot
σ	360.6	9	2726	ហ	AAH78337	337 Nucleot
σ	3	•	984	w	AAZ99946	Aaz99946 Nucleotid
7	347.6	ŗ	977	ω	999	Nucleot
œ		10.9	1085	ω	9996	N
φ	•	9	23449	w	AAZ35393	5393 Maiz
10	125.6	•	2307	ω	9993	99938 DNA e
11	٠	•	2307	9	80	7807 Rice DNA
12	•		1120	w	9994	9941 Nucleot
13	124		1087	w	AAZ99940	9940 Nucleoti
14	•		2304	ø	\vdash	8218
15	•		2655	7	ADA71289	128
16	•		3015	N	w	5639 Rice typ
17	•	٠	1036	ω	993	9939 Nucl
18		٠	2968	ம	AAH78342	n78342 Nucleoti
19		٠	3039	თ	ABK15494	5494 Wheat
20			1267	φ	ADC08721	Adc08721 Wheat DNA
21	120.6	٠	636	φ	85	852 Corn
22	•		2640	N	960	0961 D
23	•	9.0	2665	N	AAT69729	Aat69729 Plasmid p

ALIGNMENTS

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AAX34650
ID AAX3
XX Star
XX AAG1
XX WSBE
XX AAG1
XX AAG1
XX AAG1
XX AAG1
XX AAG2
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Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS; starch branching enzyme; starch soluble synthase; debranching enzyme; endosperm; wheat; barley; granule-bound synthase; glutenin; starch; grain softness protein I; bacterial isoamylase; glycogen synthase; wSBE I-D4 gene; ss.

Aegilops tauschii.

WO9914314-A1

25-MAR-1999.

11-SEP-1998; 98WO-AU000743.

12-SEP-1997; 20-MAR-1998; 97AU-00009108. 98AU-00002509.

(CSIR) COMMONWEALTH SCI & IND RES ORG.
(AUSU) UNIV AUSTRALIAN IAT.
(GCOD-) GOODMAN FIBELDER LITD.
(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

Li Z, Morell M, Rahman S;

WPI; 1999-229525/19.

New isolated cereal plant enzyme genes used for, antisense sequences of granule bound synthase. e.g. expression

Claim 8; Page 75-81; 171pp; English.

The invention relates to a novel enzyme of starch biosynthetic pathway in a cereal plant, where the enzyme is selected from starch branching enzyme (SBB) I. SBE II. starch soluble synthase (SSS) I, and debranching enzyme (DBB), with the proviso that the enzyme is not SSS I of rice, or SBE I of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rice or maize. The methods and products can be used for targeting expression specifically to the endosperm of the seeds of cereal plants such as wheat or barley. They can be used for the expression of e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low mol. wt. glutenin, grain softness protein I, bacterial isoamylase, bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be used for modifying the characteristics of starch produced by a plant. The present sequence represents the SBE II gene sequence. (Updated on 17-OCT-2003 to standardise OS field)
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Local Similarity 100.0%; )
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                                GCTATTTCTTAATCAGGTGGCCTTGGACTCTGACGATGCACTCTTTGGTGGATTCAGCAG
                                               GCTATTTCTTAATCAGGTGGCCTTGGACTCTGACGATGCACTCTTTGGTGGATTCAGCAG
                                                                                              AGTTTTAGAGCAGCCCCATTTGGACAATTGGCTGGGTTTTTGTTAGTTGTGACAGTTTCT
                                                                                                                   AGTTTTAGAGCAGCCCCATTTGGACAATTGGCTGGGTTTTTGTTAGTTGTGACAGTTTCT
                                                                                                                                                             CTCAGTTGGACTCGGTCTAATACTAGAACTATTTTCCGAATCTACCCTAACCATCCTAGC
                                                                                                                                                                                                                            TTTAATTCCACATGGATAGAGTTTGTTGGTCGTGCAGCTATCAATATAAAGAATAGGGTA
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                                                                            Nucleic acids encoding wheat starch branching altering the amylose and amylopectin content and barley.
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                                                                                                                                                                                WPI; 2001-570635/64.
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(GOOD-) GOODMAN FIELDER LTD.
(LIMA-) GRP LIMAGRAIN PACIFIC PTY )
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Example 1; Fig

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New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved
                                                                                                                                                  Zhu T, Che
Glazebrook
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Katagiri F
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Kreps J,
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Matches 370;
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                                                                                                           Wheat; starch branching enzyme II; SBEII; SBEII-2; gelatinisation onset; transgenic plant; foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention, in the area of plant biotechnology, relates to novel
                                                                                Triticum aestivum
                                                                                                                                                               Nucleotide sequence
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                                                                                                                                                                                                                                                                AAZ99942
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100.0%;
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Pred. No.
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bakery product;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gelatinization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 979 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch
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                        CCCGTGCGCT
                                                           CTGAACCCTCCTATCTTGCACATTCCCCGGTTGTTTTTGTACATATAACTAATAATTG
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CCCGTGCGCT 927
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99.5%;
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;.8e-105;
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Query Match
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Matches 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes wheat starch branching enzyme 9, designated BEIIa. The specification describes BEIIb BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding wheat starch branching altering the amylose and amylopectin content of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2726
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(GOOD-)
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GOODMAN FIELDER LTD.
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                                CCCGTGCGCTCAACGTGAAAA 1341
                                                                                                       CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
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CCCGTGCGCTCAACGTGAACA
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amylopectin; amylose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 360.6; DB 5;
Pred. No. 1.5e-102;
0; Mismatches 4;
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated stargelatinization onset and/or peak temperature.
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                                                                                                                                                                                                                                                                                                                                  Sequence 984 BP; 268 A; 212 C; 250 G; 254 T; 0 U; 0 Other;
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                                      738
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                          GAACATCCGCATGACAACAGGCCGCGCTCTTCTCGGTGTACACTCCGAGCAGAACTGCG
                                                                                                                                                                                 GTCGTGTATACCACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 984
                                                                                                                                                                                                                   GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
                                                                                                                                                          GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCTGCTTGTTACAAGGCAAAGAGAGAAA
CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATAG
                                                                                               CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGGCAACGGCGCGAGGCTGCTCTAAG
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                                      CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGAGGAGGAGCAGATGGATAG
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                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                           26.8%; Score 360; DI
98.2%; Pred. No. 1.30
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I; SBEII-1;
foodstuff;
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                                                                                                                                                                                                                                                                                                         Length 984;
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bakery p
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Matches 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gelatinisation
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 168-169; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                gelatinization
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GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
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                                                                                                977 BP; 270 A; 200 C; 245 G; 262 T; 0 U; 0 Other;
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             branching enzyme II; SBEII; SBEII-1;
n onset; transgenic plant; foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BREEDING INT CAMBRIDGE
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                                         Score 347.6; DB 3;
Pred. No. 1.1e-98;
0; Mismatches 14;
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The present sequence represents the consensus sequence of wheat starch branching enzyme II (SBEII). The specification describes novel subclasses of SBEII, designated SBEII-1 and SBEII-2. The SBEII-1 genes are thought to have similar functional properties to the maize SBEIIb gene. Starch branching enzymes catalyse the formation of the alpha-1, 6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4 glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the
                                                                                                                                                                                                                  DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2 gelatinisation onset; transgenic plant; foodstuff; bakery product;
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                                                                                                                                                                         Disclosure; Page 187; 197pp; English.
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/number= 1 306519659	29653176 /*tag= 1	29332936 /*tag= j	MECUTIONICAM ACTION	box, motif essent	7 ". ay = 9 2838 2844 /****	2831 2836 /** 287	7 ". C B J = G	ion of metallothionein genes .2671	yox,	comoters"	<pre>/*tag= c /note= "Hex, conserved element found in plant histone</pre>	/note= "Ry repeat, distal regulatory element" 19671973	/note= "I box, conserved in kBCS genes" 14751481 /*rag= b	*tag= = 1	Location/Qualifiers		<pre>ng enzyme IIb; amylose-extender gene; Ae gene; maize; corn; sssion control element; endosperm; transgenic plant; ss.</pre>	extender (Ae) gene encoding starch branching enzyme.	rst entry)		rd; DNA; 23449 BP.		511	448	CTACCGTGTTGGGTGTTTCAAGCCTGGGAAGTACAAGGTGGTCTTAGACTCCGACGCTGG 505		CCTCAAAAAAAACHTTGGTATTTGTTTCAACTTCCACITGGACTAATAACTTTTTTGA 382 		GTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCAT 322	10.35; SCOLE 146; DB 3; DELIGHT 1003; ity 86.6%; Pred. No. 6.5e-35; Indels 0; Gaps 0; servative 0; Mismatches 25; Indels 0; Gaps 0;	5 C; 284 G; 348 T; 0 U; 0 Ot	processing a foodstuff, particularly bakery products
되 되 다 다	ㅋㅋㅋ	LL LL	77. 71.	1 11 1 1 1 1 1	1 H 1	# # ! # # !	된 년 구 년 :	1 H H	1 7 7	111	H H	44.4	ኳ ካ ካ ጉ ጉ	1 13 14	g 'F) '	7 7 7 7 12 •	1 7 7 7 1 1	FIT	FT	FT	# # ! 	1 1 1 1 1 1 1	#T.	H H H	1 T T	# # # H H	13 73 74 13 14 14	1 1 1	17.7	1 H H H	1 T T	LL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of the maize amylose-extender (Ae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 98-105; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New gene regulatory sequences from plants used to provide resistance to microbial path pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ99938 standard; DNA; 2307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; gelatinisation onset; transgenic plant; foodstuff; bakery product; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding part of starch branching enzyme II clone 5A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum.
                      10-SEP-1998;
                                                                            09-SEP-1999;
                                                                                                                                 23-MAR-2000
                                                                                                                                                                                         WO200015810-A1.
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                                                                                                                                                                                                                                                             /transl_except= (pos: 2036 .2038 , a. /transl_except= (pos: 2051 .2053 , a. /transl_except= (pos: 2090 .2092 , a. /transl_except= (pos: 2096 .2098 , a. /transl_except= (pos: 2144 .2114 , a. /transl_except= (pos: 2147 .2114 , a. /transl_except= (pos: 2168 .2170 , a. /transl_except= (pos: 2168 .2170 , a. /transl_except= (pos: 2189 .2191 , a. /transl_except= (pos: 2189 .2191 , a. /transl_except= (pos: 2267 .2269 , a. /transl_except= (pos: 2306 .2272 , a. /transl_except= (pos: 2306 .2307 , a. /transl_except= (pos: 2306 .2007 , a. /transl_except= (pos: 2306 .2007
                            98EP-00307337
                                                                              99WO-GB003011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                     amino acid; the sequence codons, but no termination
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Guiltinan MJ,

Kim K;

(UYPE-) UNIV

PENNSYLVANIA STATE

12-JUN-1998; 12-JUN-1998;

99WO-US013266. 98US-0089049P. 98US-0089050P. WO9964562-A2 16-DEC-1999.

11-JUN-1999;

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RESULT 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature.
                                                                                                                                                                                                                                                                                                           plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; c tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal gr
                  22-JUN-2001; 2001US-0300112P
26-SEP-2001; 2001US-0325277P
20-DEC-2001; 2001US-0342327P
                                                                                                                                                                                                                                            Oryza
                                                                                                                                                                                                                                                                                    gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldsbrough A,
                                                                                                            21-JUN-2002;
                                                                                                                                                       03-JAN-2003
                                                                                                                                                                                                 WO2003000905-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC07807;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTT
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Pred. No. 2.9e
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                                           10-SEP-1998;
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This invention, in the area of plant biotechnology, relates to novel CC polynucleotides comprising a nucleotide sequence encoding a protein which CC is involved in or associated with the synthesis, metabolism or CC degradation of carbohydrates in the plant grain and the expression of CC which is up-regulated during grain filling. The plant is selected from CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, CC sugarbeet, wheat, and rice. The invention may be useful for the CC improvement of protein, oil, starch, fibre and moisture content of the CC cereal grains. In addition, carbohydrate levels may be modified to a more CC desirable level using the present invention. The present sequence is a CC DNA sequence encoding a rice protein of the invention. Note: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
                                                                                                       Wheat; starch l gelatinisation
                                                                                                                                                                                     Nucleotide sequence of starch branching enzyme II clone B10.
                                                                                                                                                                                                                                                                                                                                                            AAZ99941 standard; DNA; 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 73; 130pp; English.
WO200015810-A1
                                                      Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2307 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-229341/22.
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Similarity 86.7%;
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ook J, Katagiri E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTATCGCGTCGGTTGTTTAAAGCCCTGGAAAGTACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCGAGAGAGATTTGGTATTCGTGTTCAACTTCCACTGGAGTAATAGCTATTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCATGACATCTGAGCACCAGTATATATCGCGCAAACACGAGGAGGATAAGGTGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                 (first
                                                                                                       branching enzyme II; SBEII;
n onset; transgenic plant; fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                608 A; 465 C; 620 G;
                                                                                                                                                                                                                                              entry
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Kreps J, Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124.4;
Pred. No. 7e-2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   614 T; 0 U; 0 Other;
                                                                                                             foodstuff; bakery |
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Ricke D;
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                                                                                                             product;
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(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD

98EP-00307337. 99WO-GB003011.

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a clone of wheat starch branching enzyme II (SBEII), which is part of a novel subclass of known SBEII genes, designated SBEII-1, subclass B. The specification also describes subclass SBEII-2 sequences. The SBEII-1 genes are thought to have similar functional properties to the maize SBEII genes. Starch branching enzymes catalyse the formation of the alpha-1, 6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1, 4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polygeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature.
                                                                                                                                                                                             Wheat; starch branching enzyme II; SBEII; SBEII-1;
gelatinisation onset; transgenic plant; foodstuff;
                                                                                                                                                                                                                                               Nucleotide
                                                                                                                                                                                                                                                                                                           AAZ99940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1120 BP; 338 A; 208 C; 252 G; 308 T; 0 U; 14 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                processing a foodstuff, particularly bakery products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 123-124; 197pp; English.
                                                                                                                                                                   Triticum aestivum
                                                                                                                                                                                                                                                                            25-JUL-2000
                                                                                                                                                                                                                                                                                                                                        AAZ99940 standard;
                                                                        09-SEP-1999;
                                                                                                       23-MAR-2000.
                                                                                                                                    WC200015810-A1.
            (PLAN-) PLANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTATGACATCAGACCAGCTACGTTTCTCGGAAACATGAGGAAGATAAGGTGATCGTG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTTGCCTTTTCATTGTCCA 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGGAAGATAAGGTGATCATC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCGGGTCGGCTGTTTAAAGCCTGGGAAGTACAAGGTGGTCTTAGACTCGGACGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                            (first
            BREEDING INT CAMBRIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                      509
                                                                                                                                                                                                                                                                                                                                                                                                                                                  448
                                           98EP-00307337.
                                                                        99WO-GB003011
                                                                                                                                                                                                                                                                                                                                        DNA; 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.2%;
                                                                                                                                                                                                                                              of starch branching enzyme
                                                                                                                                                                                                                                                                           entry)
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Pred. No. 5.2e-28;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                           ΒP
              CLT
                                                                                                                                                                                                                                               II clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1120;
                                                                                                                                                                                               starch; SBEII-2;
bakery product;
                                                                                                                                                                                                                                                 B.4
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RESULT 14
ADCO8218
ID ADCO82
XX ADCO8
XX DIGGEORY
AC ADCO8
XX 18-DE
XX Plant
KW Carbb
KW Carb
KW Weane
XX Weene
XX Weene
XX WO200
XX W22-J
PR 21-JI
XX 22-JJ
PR 26-JJ
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a clone of wheat starch branching enzyme designated SBEII-1, subclass C. The specification also describes subclass SBEII-2 sequences. The SBEII-1 genes are thought to have similar functional properties to the maize SBEIIb gene. Starch branching enzymes catalyse the formation of the alpha-1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particularly backery products processing a foodstuff, particularly bakery products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature.
                                                                                                                                                                                                                                                                                    carbohydrate degradation; carbohydrate; plant grain; grain filling; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
                                                                                                                                                                                                                                                                                                                    plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
                                                                                                                                                                                                                                                                                                                                                         Rice
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                                                                                                                                                                                                                     Oryza sativa
                                                                                                                                                                                                                                                    wheat; rice; protein; oil; starch;
gene; ds; plant.
                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2003
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                                                                                                                   21-JUN-2002; 2002WO-IB002450
                                                                                                                                                     03-JAN-2003.
                                                                                                                                                                                     WO2003000905-A2
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                                                                                                                                                                                                                                                                                                                                                       DNA sequence Seq ID523 related to grain filling.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTT 427
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.2%;
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Pred. No. 5.9e-28;
0; Mismatches 25
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                                                                                                                                                                                                                                                                      tibre; moisture content;
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22-JUN-2001; 2001US-0300112P. 26-SEP-2001; 2001US-0325277P. 20-DEC-2001; 2001US-0342327P.

(SYGN)

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PARTICIPATIONS

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                                                                                                                                                                                                                                                                                                                                                             RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
                                                                                                                                                                       Oryza
                                                                                                                                                                                                                                            Rice gene,
                                                                                                                                                                                                                                                                                                     ADA71289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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Glazebrook J,
                                                      22-JUN-2001; 2001WO-IB001105
                                                                                    22-JUN-2001; 2001WO-IB001105
                                                                                                                03-JAN-2003
                                                                                                                                            WO2003000898-A1
                                                                                                                                                                                                  gene,
                                                                                                                                                                                                                 Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                                                                                                                ADA71289 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2304 BP;
                            (SYGN ) SYNGENTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCGAGAGAGAGTTTGGTATTCGTGTTCAACTTCCACTGGAGTAATAGCTATTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCATGACATCTGAGCACCAGTATATATCGCGCAAACACGAGGAGGATAAGGTGATCATC
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                            PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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Similarity 84.2%;
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 TATCGCGTCGGTTGTTTAAAGCCTGGAAAGTACAAGATTGTGTTG
                                 TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTG
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0 4 US-09-087-277-1
0 4 US-09-257-894-19
1 US-09-257-894-12
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Sequence 602, Appli Sequence 4, Appli Sequence 4, Appli Sequence 94, Appl	1720	Sequence 3, Appli Sequence 1, Appli Sequence 252, App	Sequence 53, Appl Sequence 53, Appl Sequence 49, Appl Sequence 3, Appli	

ALIGNMENTS

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LENGTH: 2853
; TYPE: DNA
; ORGANISM: Triticum aestivum
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(2499)
; OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-3
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APPLICANT: Willmitzer, et al.

TITLE OF INVENTION: NUCLECTRATION AND COMPOSITION IN PLANTS

TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS

FILE REFERENCE: 514413-3515.1

CURRENT FILING DATE: 2000-06-30

CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: PCT/EP92/00302

PRIOR APPLICATION NUMBER: PCT/EP92/00302

PRIOR FILING DATE: 1992-02-11

NUMBER OF SEQ ID NOS: 4

SOPTWARE: Patentin version 3.0

SEQ ID NO 3
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APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccarides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
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Matches 149;
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Patent No. 6639126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (2)...(2446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: SBEIIa
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ORGANISM: Zea mays
                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Genbank Accession No. 6639126 U65948
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                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2298
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              OKUPALLE

F: Broglie, Kare...
T: Klein, Theodore M.
T: Klein, Theodore M.
T: Hubbard, Natalle L.
NT: Lightner, Jonathan E.
NT: Lightner, Jonathan E.
PINVENTION: No. 6376749el Starches via Modification of DF INVENTION: Expression of Starch Biosynthesis
THIVENTION: 25, THE STATE OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTTTTC 2305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCCTTC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cccgrecect 1330
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1007 Market Street
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Pred. No. 3.5e-30;
0; Mismatches 39
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NAME/KEY:
LOCATION:
US-09-257-894-1
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Best Local Similarity
Matches 138; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-92-4926
TELEPHONE: 302-92-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0:
FILING DATE: JUNE 10,
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: JUNE 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Majarian, William R.
REGISTRATION NUMBER: 41,17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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2282
                                                                                                                                              2162 AATTCATGACATCTGATCACCAGTATATTTCCCGGAAACATGAGGAGGATAAGGTGATTG
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                                ACTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTG 428
                                                                                                           TCCTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTG
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ACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTGGTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2665 base pairs
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Pred. No. 1.6e-28
                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                        Length 2665;
2328
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RESULT 4
US-09-731-166-11
US-09-731-166-11
Sequence 11, Application US/09731166
Patent No. 6639126
Patent No. 6639126
Patent No. 6639126
Patent No. 6639126
Patent No. Family Vincent J. H.
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccarides
PILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SOFTWARE: FASTSEQ for WINDOWS Version 4.0
SEQ ID NO 11
LENGTH: 2720
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
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RESULT 5
US-08-941-445A-14
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Best Local Similarity 82.6%;
Matches 138; Conservative
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APPLICANT: Keeling
APPLICANT: Guan, 1
                                                                                                                                                                                                                              TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Genbank Accession No. 6639126 AF072725 NAME/KEY: CDS LOCATION: (101)...(2500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (0)...(0) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan,
STREET: 5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                            NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 499-8880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-SEP-1
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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MEDIUM TYPE: Floppy disk
                                                                                                         ORIGINAL SOURCE
                                                                                                                         MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Starch Encapsulation NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                      TELEPHONE: (303) 499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 5370 |
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                 ORGANISM:
                                       NAME/KEY:
                                                                                                                                                                     TOPOLOGY:
                      OCATION:
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                      sig_peptide
91..264
                                                                                 Zea mays
                                                                                                                                                                     not relevant
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Pred. No. 1.6e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-48
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
BARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SECTION OF SEQ ID NOS: 4
SECTION PROPERTY OF SEQ ID NOS: 4
SECTION OF SEQ ID NOS: 4
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LOCATION:
US-08-941-445A-14
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Best Local Similarity 82.6%;
Matches 138; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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LOCATION:
FEATURE:
NAME/KEY:
FEATURE:
NAME/KEY: misc feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa =
OTHER INFORMATION: or Phe.
                                                                                                 NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897
OTHER INFORMATION: n wherein n = A, C, G or T.
                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (189)..(2825)
                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Unknown OTHER INFORMATION: (branching enzyme II) forther Information: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3074
TYPE: DNA
                                                                                                                                                                                                               NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
                                                                                                                                                                                                                                                                          NAME/KEY: sig_peptide
LOCATION: (189)..(332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2234 TETTCGÁÁÁAGGGÁGÁTTTGGTÁTTTGTGTTCÁÁCTTCCÁCTGCÁACÁÁCAGCTATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2174 AATTCATGACATCTGATCACCAGTATATTTCCCCGGAAACATGAGGAGGATAAGGTGATTG 2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2294 ACTACCGTATTGGTTGTCGAAAGCCTTGGGGTGTATAAGGTGGTCTTG 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 AGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCA
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265..2487
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0; Mismatches
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                                                                                                                                  and 2156 are
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                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR FILING DATE: 1995-11-29
PRIOR FILING DATE: 1995-11-29
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR APPLICATION NUMBER: SE 9601506-0
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                                                                                                                      PRIOR FILING DATE: 1996.
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver.
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application Patent No. 6469231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid
-09-087-277-1
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME
FILE REFERENCE: 003300-486
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LARSSON, APPLICANT: LARSSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: EK,
APPLICANT: KHO
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LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
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NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino
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 OTHER INFORMATION:
OTHER INFORMATION:
                                                   TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                         ENGTH: 3074
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Local Similarity 67.9%;
les 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       RASK, Lars
                                                                                                                                                                                                                                                                                                                                                                                                     LARSSON, Hakan
                                                                                                                                                                                                                                                                                                                                                                                                                         KHOSNOODI, Jamshid
LARSSON, Clas-Tomas
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Description of Unknown Organism:beII gene (branching enzyme II) from Solanum tuberosum (potato)
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                                                                                                                                            2.0
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Pred. No. 7.8e-19;
0; Mismatches 60
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GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
ITILE OF INVENTION: Production of Modified Polifile REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER: FastSEQ for Windows Version 4.0
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US-09-731-166-13
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Best Local Sim
Matches 127;
                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09731166 Patent No. 6639126
                                                                                                                     SEQ ID NO 13
                    FEATURE: FEATURE: NAME/KEY: misc_feature
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LOCATION:
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LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid 522 is
OTHER INFORMATION: or Phe.
NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Nucleotides 92,
OTHER INFORMATION: n wherein n = A,
NAME/KEY: misc feature
LOCATION: (285)...(287)
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OTHER INFORMATION: Amino
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LOCATION: (333)..(282)
                                                                       ORGANISM: Zea mays
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LOCATION: (1428)..(143
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            DTHER INFORMATION:
NAME/KEY:
                                                                                                   ENGTH:
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INFORMATION: Amino
                                                                                       DNA
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(189)..(332)
                                                                                                                                                                                                                                                                                                                                                                                              CACTTTT 2635
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              Genbank Accession
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7.8e-19;
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               NO.
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; LOCATION: (2)...(2470) US-09-731-166-13

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                                     US-09-257-894-19
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: Microsoft Windows 95 SOFTWARE: Version 7.0A CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/257,894 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.3%;
Best Local Similarity 56.9%;
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19,
Query Match
                                                                                                                                                                 TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: JUNE 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                        MOLECULE TYPE:
                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION: Expression of Starches via Modification ITLE OF INVENTION: Expression of Starch Biosynthesis ITLE OF INVENTION: Enzyme Genes
                                                                                                                                                                                                                                       NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                       STRANDEDNESS:
                                                                                                                                                                                                   TELEPHONE:
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6376749
                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilmington
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1007 Market Street
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Klein, Theodore M.
                                                                                                                                                                                                       302-992-4926
                                                                                       single
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Pred. No. 2.8e-08;
0; Mismatches 81;
   Score 58.4;
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Length 2470;
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                                                                      US-09-257-894-24
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Patent No. 63767
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 Matches 107;
                Query Match
Best Local Similarity
                                                                                                                                                                        TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,
PILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41, 173
REFERENCE/DOCKET NUMBER: BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification
TITLE OF INVENTION: Expression of Starch Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100, ....
CITY: Wilmington
                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: Microsoft Windows SOFTWARE: Version 7.0A
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Delaware COUNTRY: USA
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                                                                                                                                                           LENGTH:
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                                                                                                                                                           2565 base pairs
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1007 Market Street
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Klein, Theodore M.
                56.9%;
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                                                                                                                                                                                                                                                                               41,173
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Score 58.4; DB 4;
Pred. No. 2.9e-08;
0; Mismatches 81;
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0; Mismatches 81; Indels
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                                   Length 2565;
     Indels
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                             US-08-941-445A-16
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                                                                                                                                                                                                                                                                                             TELEPAX: (303) 499-8089
[INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/941,445;
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA: 80
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                   HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 50 CITY: Boulder CO
                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                TOPOLOGY: no
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                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Winner, Ellen P
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                    ORGANISM:
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                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                              TRANDEDNESS:
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                                                                                                                                                                                                                                                                              nucleic acid
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4.3%;
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Score 58.4;
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DB 3;
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Length 2763;
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Query Match

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RESULT 12
US-09-257-894-12
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                                                                                                   ; LOCATION:
US-09-257-894-12
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/09.
APPLICATION NUMBER: 10, 199.
ATTORNEY/AGENT INFORMATION:
ANAME ANAME TO THE TOTAL T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BB
                                                                                                                                                                                                                                       HOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2175
                                                                                                                                                                                                                                                                                                           TRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ATGAGGAAGATAAGGTGATCATCCTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19898
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                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGCCCTGGACTCTGATGCTCTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGG 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCCAAGAAAACTTACGAGGGCTACAAAGTGGGATGCGATTTGCCCTGGGAAATACAGAG 2114
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                    2772 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hubbard, Natalie
Lightner, Jonatha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Klein, Theodore M.
                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302-992-4926
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Enzyme Genes
4.3%;
56.9%;
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   Score
Pred.
   58.4; DB 4;
No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Starches via Modification of Starch Biosynthesis
                                Length 2772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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US-09-257-894-2/c
                                                                                                                                                      , MOLECULE TYPE:
US-09-257-894-2
                                                                                                                                                                                            TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Broglie
APPLICANT: Klein,
APPLICANT: Hubbard
APPLICANT: Lightne
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                                                                 Query Match 4.1%;
Best Local Similarity 80.2%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
APPLICATION NUMBER: 09/091,052
APPLICATION NUMBER: 09/091,052
APPLICATION NUMBER: MAME: MAME: MAJERIAN, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECHONE: 302-992-4926
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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348 GTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGACTACCGTGTTGGGTGTTCCAAGCCT
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    E. I. du Pont de Nemours and Company
1007 Market Street

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Klein, Theodore M.
                                                                                                                                                                          DNA (genomic)
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                                                                     0
                                                                   Score 55.4; DB 4;
Pred. No. 8.1e-08;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95
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                                                                                                         Length 414;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Particle PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/104,158
FILING DATE: 13-AUG-1993
CLASSIFICATION NUMBER: US/08/104,158
FILING DATE: 13-FEB-1992
PRIOR APPLICATION NUMBER: EP PCT/EP92/00302
PRIOR APPLICATION NUMBER: B PCT/EP92/00302
PRIOR APPLICATION NUMBER: B P 41 04 782.6
PRIOR APPLICATION NUMBER: DE P 41 04 782.6
PRIOR APPLICATION NUMBER: DE P 41 04 782.6
PRIOR APPLICATION NUMBER: DE P 41 04 782.6
PRIOR APPLICATION NUMBER: PA 1996
PRIOR APPLICATION INFORMATION:
TELEPHONE: 212-382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-104-158-1
                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212-382-0700
TELEFAX: 212-382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2909 base pairs
TYPE: mucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 1, Application US/08104158
Patent No. 6215042
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APPLICANT: Wil
                                                                                                                                                                                                  MOLECULE TYPE: C
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sola
FEATURE:
NAME/KEY:
LOCATION:
                                                        TISSUE TYPE: tuber
CELL TYPE: total tuber
IMMEDIATE SOURCE:
LIBRARY: CDNA of total
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APPLICANT: Jacobsen, Evert
TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                              STRAIN: Desiree
DEVELOPMENTAL STAGE:
TISSUE TYPE: tuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York COUNTRY: U.S.A. ZIP: 10036-8403
                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 GTGTTCAACTTCCACTGCAACAACAGCTATTTTGACTACCGTATTGGTTGTCGAAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T: 1180 Avenue of the Americas
Nork
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Kossmann, Jens
Mueller-Roeber, Bernd
Visser, Richard Gerardus Francisus
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CDS
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                                                                      tuber mRNA in
                                                                    pUC 19 (Hinc
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GENERAL INFORMATION:

APPLICANT: Willmitzer, et al.

APPLICANT: Willmitzer, et al.

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE

TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS

FILE REFERENCE: 514413-3515.1

CURRENT APPLICATION NUMBER: US/09/609,040

CURRENT APPLICATION NUMBER: PCT/EP92/00302

PRIOR APPLICATION NUMBER: PCT/EP92/00302

PRIOR FILING DATE: 1992-02-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 2909

TYPE: DNA
ORGANISM: Solanum tuberosum

PEATURE:
NAME/KEY: CDS
LOCATION: (2)...(1699)

COTHER INFORMATION: BRANCHING ENZYME

US-09-609-040-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-104-158-1
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US-09-609-040-1
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Search completed: April 10, 2004, 14:13:17 Job time : 100.567 secs
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Best Local Similarity 58.9%;
Matches 93; Conservative
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Best Local Similarity
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                                                                                             1986 TATAAAGTTGGATGTGACTTGCCAGGGAAGTACAGAGT 2023
                                                                                                                                                                                                                                                                                            1866 TTCCTCGCATCAGGAAAACAGATAGTAAGCAGCATGGATGATGATAATAAGGTTGTTGTG 1925
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                                                                                                                                           384
                                                                                                                                                                                                                            324 CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC 383
                                                                                                                                                                                                                                                                                                                     264 TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGGAAGATAAGGTGATCATC 323
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                                                                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                         TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGT 421
                                                                                                                                                                                              TTTGAACGTGGTGACCTGGTATTTGTATTCAACTTCCACCCAAATAACACATACGAAGGG 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATAAAGTTGGATGTGACTTGCCAGGGAAGTACAGAGT 2023
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ilarity 58.9%;
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(partial) truncated protein; 97,11 % identity to
active potato branching enzyme"
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Pred. No. 8.6e-07;
0; Mismatches 65
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Minimum DB seq
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Published Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*
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length: 2000000000
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1344
1 tragatatogtggtatgcaa.....tgcgctcaacgtgaaaatcc 1344
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10621.793 Million cell updates/sec
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

14 12	2529 14	2418 11	2418 9	602 9	8.0 1642 15	119.6 8.9 2780 12	9.0 636 15	122.4 9.1 1267 15	122.6 9.1 3039 9	122.6 9.1 2559 9	19.6 2554 12	1119 15	11476 12	Result Query No. Score Match Length DB ID
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Sequence 13, Appl Sequence 8329, Ap	Sequence 17, Appl	Sequence 872, App	Sequence 872, App	Sequence 955, App	Sequence 1027, Ap	Sequence 2, Appli	Sequence 5563, Ap	Sequence 3480, Ap	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3410, Ap	Sequence 3, Appli	Description

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GGGTATGTCACTGGTTTGTCTTTGTTGCATAACAAGTCACAGTTTAACGTCAGTCTCTTC 120

GTCTTTGTTGCATAACAAGTCACAGTTTAACGTCAGTCTCTTC 10251

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US-10-242-535A-14106	-10-085-783A-1410	-10-242-535A-5414	10-085-783A-5	-10-425-114-11503	-10-369-493-276	-10-369-493-254	-10-397-954A-1	-10-424-599	-10-102-524-	-10-240-96	-10-084-817-92	-10-262-511-10	-09-918-624B-3	09-880-107-214	0-342-887	-10-235-192	2	-10-425-114	938-842A-337	09-938-842A-33	-10-393-840-26	-10-056-454A-1	056-454A	56-454A-1	0-254-534-1	-10-056-454A-	-10-056-454A-1	8-3	
0	e 14106,	54140,	1 U	11505,	0 27656,	e 25407,	1, Appl	141092,	16	135, Ap	92	10	e 30	214	Sequence 44	e 36	N	32	e 337,	337	26	quence 14	equence 12, App	18	eguence 1,	equence 19	equence 16	equence 3,	

ALIGNMENTS

RESULT 1 US-10-434-893A-3

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                                                                                                                                                                                                    ; OTHER INFORMATION: SSBEIIa gene US-10-434-893A-3
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Publication No. US20040060083A1
PUBLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and TITLE OF INVENTION: containing products with an increased amylose content FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 2:1
                                                                                                Query Match 99.2
Best Local Similarity 99.9
Matches 1344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3
                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANIAM: Aegilops tauschii
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(11476)
OTHER INFORMATION: n is a, c, g or t
                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 11476
10132 TTAGATATCGTGGTATGCAAGAGTTCGATCAGGCAATGCAGCATCTTGAGGAAAAATATG
                                               TTAGATATCGTGGTATGCAAGAGTTCGATCAGGCAATGCAGCATCTTGAGGAAAAATATG
                                                                                                   99.2%; Score 1333; DB 12;
99.9%; Pred. No. 0;
Live 0; Mismatches 0;
                                                                                                                                                  Length 11476;
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Db 1027 CIGAACCCICCTATCTIGCACATICC	
1261	1140 GCGCCATGACTGGGAGGGGATCGTGCCCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATA 1199 1
QY 1201 GTAGCTTGTTGGTGAGCGCTCGAAAGAAA	1 1
Qy 1141 CGCCATGACTGGGAGGGGATCGTGCCTCT	GGTCGTCTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTTACAAGGCAAAGAAGAAAAA GGTCGTCTATGCCCTTACAAGAGTAAGAAACCAGCGGCTTGTTACAAGGCAAAGAGAGAA 1 GGTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCAGCGGCTTGTTACAAGGCAAAGAGAGA 1
QY 1081 CTCCAGAGAGCTCGTGGATCGTGAGCGAA	GGAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGC 1
QY 1021 GTCGTGTATGCCCTTACAGAGTAAGAACC	P — P
Qy 961 GAACATCCGCATGACAACAGGCCGCGCTC	C - 89
Query Match Best Local Similarity 100.0%; Pred. No. Matches 370; Conservative 0; Mismatc	
	10
	660 GCTCAGTTGGACTCGGTCTAATACTAGAACTATTTTCCGAATCTACCCTAACCATCCTAG 719
PRIOR APPLICATION NUMBER: US 60/325,448 PRIOR FILING DATE: 2001-09-26 PRIOR APPLICATION NUMBER: US 60/325,277 PRIOR FILING DATE: 2001-09-26	600 GCCCGAAGCACATACCATTCATTCATATTATCTACTTAAGTGTTTGTATCCAATCTTTAT 659
PPL	540 AATTTGTAAAGAAAGAATTTGCTCGAGCTGTTGTAGCCATAGGAAGGTTGTTCTTAACA 599
 22 25 2	480 TTTTAATTCCACATGGATAGAGTTTGTTGGTCGTGCAGCTATCAATATAAAGAATAGGGT 539
	420 GTATGCTTGCCTTTTCATTGTCCACCCTTCACCAGTAGGGTTAGTGGGGGGCTTCTACAAC 479
ORMAT Budw Mou Bri	360 CACTGGAGCAATAGCTTTTTTGACTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAG 419
RESULT 2 US-10-260-238-3410 ; Sequence 3410, Application US/10260238 ; Publication No. US20040016025A1	301 ATGAGGAAGATAAGGTGATCATCCTC-AAAAGAGGAGATTTGGTATTTGTTTTCAACTTC 359
11452 GCCCGTGCGCTCAACGTGAAAATCC 114	241 CAGCACTGACAATGTAACTGCAGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAAC 300
11392	181 AGCTGGAATTGCTTTTCACCAAAACTATTTTCTTAAGTGCTTGTGTATTGATACATATAC 240
11332 GGTA	121 AAGTGGTAAAAAAAGTGTAGAATTAATTCCTGTAATGAGATGAAAACTGTGCAAAGGCGG 180
2y 1200 GGTAGCTTGTTGGTGAGCGCTCGAAAGAA	

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CTTTCTCGGTGTACACTCCGAGCAGAACTGCG 1020
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tches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                  ATION OF PLANT EXPRESSION
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                                176
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                                                                                                       AGCGACGGGCAACGGCGCGAGGCTGCTCCAAG 1140
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RESULT 3
US-10-434-893A-1
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US-09-792-127-1
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APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch.
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 343; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
LENGTH: 2554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10434893A Publication No. US20040060083A1
                                                                                                                          GENERAL INFORMATION:
                                                                                                                                             Sequence 1, Application US/09792127 Patent No. US20020002713A1
                                                     APPLICANT: Allen, Steve
APPLICANT: Beckles, Dian
APPLICANT: Butler, Karl
APPLICANT: Beckles, Diane M.
APPLICANT: Butler, Karla
APPLICANT: Pearlstein, Rich
TITLE OF INVENTION: Starch Branching Enzyme IIb
FILE REFERENCE: BB1439 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2128 GAACATCCGCATGACAACAGGCCACGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGAA 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGGCAACGGCGGGGGGCTGCTCCAAG 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCAGTGAGCTCGTGGATTGTGAGCGAAGCGACGGGCAACGGTCCGAGACTGTTCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                GTG----TTTGTTGTGCTGCACTGAACCCTCCTCCTATCTTGCACATTCCCGGTTGTTTT 1299
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                                                                                                                                                                                                                                                                        TGTACATATAAACTAATAATTGCCCGTGCGCT 2516
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87.5%;
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Patent NO. US200202713A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Beckles, Diane M.
APPLICANT: Bearlstein, Rich
TITLE OF INVENTION: Starch Branching
FILE REFERENCE: BB1439 US NA
CURRENT APPLICATION UNMBER: US/09/792
CURRENT APPLICATION UNMBER: US/09/792
CURRENT FILING DATE: 2001-02-3
PRIOR APPLICATION NUMBER: 06/186098
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/792,12
CURRENT FILING DATE: 2001-02-23
CURRENT FILING DATE: 2001-03-01
FRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 2559
TYPE: DNA
ORGANISM: Triticum aestivum
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Best Local Simi
Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 3039
                                                                                                                                                                                                                                                                                       Query Match 9.1%; Score 122.6; DB 9; Best Local Similarity 78.9%; Pred. No. 6.5e-27; Matches 146; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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Local Similarity 78.9%;
                                                                                                                                                                                                              2256 TTTÁTGÁCATCAGACCACCAGTACGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTG 2315
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                                                                         TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTGCCTTTTCATTGTCCA 443
                                                                                                                                                        CTCAAAAGAGGGAGAITTGGTAITTGTTTTCAACTICCACTGGAGCAATAGCTITTTTTGAC 383
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      CCCTT 448
                                             TACCGGGTCGGCTGTTTAAAGCCTGGGAAGTACAAGGTGGTCTTAGACTCGGACGCTGGA
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Pred. No. 5.8e-27;
0; Mismatches 39;
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Gaps

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2435

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1776 TTTATGACATCAGACCACCAGTACGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTG
1896 TACCGGGTCGGCTGTTTAAAGCCTGGGAAGTACAAGGTGGTCTTAGACTCGGACGCTGGA
                                                                                                1836 TTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAGTAGCTATTTCGAC
                                                                                                                                 324 CTCAAAAGAGGAGATITGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC
                                             384 TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTGCCTTTTCATTGTCCA
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APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Teven P.
APPLICANT: Copper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
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PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 3480
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                                                                                                                                                                                                                                                                                     Sequence 5563, Application US/10260238 Publication No. US20040016025A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.1%;
Best Local Similarity 84.1%;
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION FILE REFERENCE: 60111-NP CURRENT APPLICATION NUMBER: US/10/260,238 CURRENT FILING DATE: 2002-09-26 PRIOR APPLICATION NUMBER: US 60/325,448 PRIOR PILING DATE: 2001-09-26 PRIOR APPLICATION NUMBER: US 60/325,277 PRIOR APPLICATION NUMBER: US 60/325,277 PRIOR APPLICATION NUMBER: US 60/325,277 PRIOR EILING DATE: 2001-09-26
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                                                        APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                              APPLICANT: Budworth, Paul R. APPLICANT: Moughamer, Todd G.
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                                     TIE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
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FERENCE: 60111-NP
APPLICATION NUMBER: US/10/260,238
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                                                                                                                                     Goff, Stephen A.
Katagiri, Fumiya
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Cooper, Bret
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Ricke, Darrell
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                                                                                Ricke,
                                                                                                    Provart, Nicholas
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                                                      Tong
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                                                                                Darrell
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                                                                                                                                         Fumiyaki
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RESULT 9 US-10-260-238-1027

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CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PILING DATE: 2001-09-26
PRIOR PPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 5563
LENGTH: 636
TYPE: DNA
TYPE: DNA
TORGANISM: Zea mays
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US-10-434-893A-2
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APPLICANT: Added Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 64925
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10434893A Publication No. US20040060083A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              Best Local
Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2780
TYPE: DNA
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2302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCA
                                                                                                                                                                                                                               264 TITATGACATOTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC 323
                                                                                                                                                                                                                                                                              tch 8.9%; Score 119.6; DB 12; Length 2780; al Similarity 84.8%; Pred. No. 5.4e-26; 134; Conservative 0; Mismatches 24; Indels 0;
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                                               TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGT 421
                                                                                         TTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAATAGCTATTTCGAC
                                                                                                                                      CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC 383
                                                                                                                                                                                     TTTATGACATCAGACCACCAGTACGTATCTCGGAAACACGAGGAAGATAAGGTGATCGTG 2241
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  TACCGGGTCGGTTGCTTAAAGCCTGGGAAGTACAAGGT 2339
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82.6%; Pred. No. 9.2e-27;
Pative 0; Mismatches 29
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GENERAL INFORMATION:

Sequence 1027, Application US/10260238 Publication No. US20040016025A1

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APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1027
LENGTH: 1642
TYPDE: NMA
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US-09-770-149-955/c
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US-10-260-238-1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 955,
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                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1341 TTATATTTGAGAAGGGAGATCTGGTATTTGTGTTCAACTTCCATTGGAGTAACAGCTATT
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US20020059663A1
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Provart, Nicholas
Ricke, Darrell
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Goff, Stephen A.
                                                                                                  Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                                                                                                                                                                                                                           An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
                                                               Davis, Keith R.
Allen, Keith
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Hoffman, Neil
Hurban, Patrick
ENTION: Expressed Sequences of Arabidopsis
                                                                                                                                                    Woessner, Jeffrey P. Haas, William David
                                                                                                                                                                                     Matthew, Abraham V.
Ledford, Brooke L.
                                                                                                                                                                                                                          Page,
                                                                                                                                                                                                                                        Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                           Raines, Tracy M.
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Pred. No. 3e-22;
0; Mismatches 38;
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US-09-938-842A-872
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                                                                                                                                                                                                                                                            SEQ ID NO 872
LENGTH: 2418
TYPE: DNA
                   2158 TTCGÁAÁGÁGGTGÁTCTCGTCTTTTÁACTTTCACTGGÁCCAGCÁGCTACTTTGÁT 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384
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Sequence 872, Application US/09938842A

Patent No. US200320160378A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
ITILE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
ITILE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/27,866
PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-06-22

NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22
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CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 955
LENGTH: 602
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; ORGANISM: Arabidopsis thaliana
US-09-770-149-955
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Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                     Query Match 7.2%; Score 97; DB 9; Le Best Local Similarity 70.3%; Pred. No. 6.4e-19; Matches 130; Conservative 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
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324 CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC
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                                                                                                                                264 TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC 323
                                                                       TTTATGACTTCGGAGCACCAATTCATATCACGAAAAGACGAAGCAGATAGAGTAATCGTA 2157
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70.3%;
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Pred. No. 2.4e-19;
0; Mismatches 55
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US-09-938-842A-872
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Publication No. US20040009476A9
                                                                                                                                                                                                                   Sequence 17, Application US/10056454A Publication No. US20030166919Al
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Best Local Similarity
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LENGTH: 2418
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-08-26
PRIOR PILING DATE: 2001-08-26
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                              GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
APPLICANT: Inprovements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2158 TICGAAAGAGGIGATCTCGTCTTTGTCTTTAACTTTCACTGGACCAGCAGCTACTTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAAAAGAGGAGGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC 383
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                CITY: Newcastle
STATE: Delaware
COUNTRY: United States of America
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ZIP: 19720

Indels

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Gaps

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US-10-056-454A-13
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                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-056-454A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/10056454A
Publication No. US20030166919A1
PUBLICAL INFORMATION:
APPLICANT: National Starch and
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Query Match 6.9%;
Best Local Similarity 68.4%;
Matches 128; Conservative 0
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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Local Similarity 69.0%;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
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                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                        LENGTH: 2975 base pairs
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Score 92.6; DB 14; Pred. No. 1.8e-17; O; Mismatches 59;
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Search completed: April 10, 2004, 20:07:39 Job time: 478.681 secs
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8329
LENGTH: 1867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.8%; Score 91.6; DB 12; Length 1867; Best Local Similarity 68.3%; Pred. No. 2.7e-17; Matches 127; Conservative 0; Mismatches 59; Indels 0;
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ORGANISM: Glycine max
FEATURE:
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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ALIGNMENTS

	source	FEATURES			•			COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	BU607192
/organism="Triticum aestivum" /mol_type="mRNA" /db_xref="taxon:4565"	1 724	Location/Qualifiers	Email: zhiwufy@sdau.edu.cn.	Tel: 086-0538-8241144	Shan dong agriculture university, Tai'an, Shan dong, China	college of life sciences	Plant development molecular biology lab	Contact: Xiansheng Zhang	Unpublished (2002)	Expressed sequence tags analysis of a wheat seed CDNA library	Li,J., Wang, F., Li,Q. and Zhang, X.	1 (bases 1 to 724)	Pooideae; Triticeae; Triticum.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Triticum aestivum	Triticum aestivum (bread wheat)	EST.	BU607192.1 GI:23270467	BU607192	1G7 wheat seed cDNA library Triticum aestivum cDNA, mRNA sequence	BU607192 724 bp mRNA linear EST 23-SEP-2002	

Result No.

Score

Query Match Length DB

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Description

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464.8 370 366.8 365.8

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BU607192 CD912768 BQ237446 CK210642

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                                               CD912768
1 G550.115M08R010903 G550 1
mRNA sequence.
CD912768
CD912768.1 GI:32687092
EST.
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Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTAGTTGTGACAGTTTCTGCTATTTCTTAATCAGGTGGCCTTGGACTCTGACGATGCA 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACACTCCGAGCAGAACTGCGGTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCAGCGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTGCTGATGCCCTTGCAGGAACATCCGCATGACAACAGGCCGCCTCTTTCTCGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTTTGGTGGATTCAGCAGGCTTGATCATGATGTCGACTACTTCACAACCGTAAGTCTG
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                                                                                                                                                                                              GTACATATAACTAATAATTGCCCGTGCGCTCAACGTGAAAAT 1342
                                                                                                                                                                                                                                                 TGGGTGTTTGTTGTGCTGCACTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTT
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                                                                                                                                                                             GTACATATAACTAATAATTGCCCGTGCGCTCAACATGAACAT
                                                                                                                                                                                                                                                                                CGGCGCGAGGCTGCTCTAAGCGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGC
                                                                                                                                                                                                                                                                                                                                                         CGGCGCGAGGCTGCTCCAAGCGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGC
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/clone_lib="wheat seed cDNA library"
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Pred. No. 1.5e-:
0; Mismatches
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                                                                                                   610 bp mRNA
Triticum aestivum
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.5e-125;
es 52; Indels
                                                                                                  linear E
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BQ237446/c
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                                                                                                      sequence.
BQ237446
BQ237446.1
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               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatephyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
1 (bases 1 to 573)
                                                                                                                                            BQ237446 573 bp mi
TaE05016F12F TaE05 Triticum aestivum
      Cloutier, S.
                                                                   Triticum aestivum
                                                                              Triticum aestivum (bread
                                                                                                         GI:20433322
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Genoplante 93, rue Henri Rochefort 91025 EVRY CEDEX France 93, rue Henri Rochefort 91025 EVRY CEDEX France 7el: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoplante, a major partnership Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG 1020
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                                 cccerececr
                                                                                               CTGAACCCTCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                                                                                     CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATAG
                                                                                                                                                                                                                                                                                                      CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGGCAACGGCGAGGCTGCTCCAAG
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CCCGTGCGCT
                                                                         CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATAACTAATAATTG
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pollination)"
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/cultivar="recital"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Triticum aestivum"
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Pred. No. 1.4e-97;
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573

CDNA

clone

linear

EST 03-MAY-2002

wheat)

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TITLE
JOURNAL
COMMENT
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CK210642
LOCUS
DEFINITION
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VERSION
KEYWORDS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wheat functional genomics - Glenlea developing seeds cDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-2340
Fax: (204) 983-2604
Email: scloutter@agr.gc.ca
was cloned directionally, not all sequences generated with reverse was cloned directionally, not all sequences generated with reverse primer ware from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 016 row: F column: 12
Seq primer: MJ3 Forward.
                                                                                                                                         CK210642 III07 bp mRNA linear EST 08-DEC-2003 FGAS022466 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
Triticum aestivum (bread wheat)
Triticum aestivum
Eukarvota: Viridivalantae: Streptophyta: Embryophyta: Tracheophyta:
                                                                                CK210642.1 GI:39573032
                                                                                                                         aestivum cDNA,
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/dev stage="5 days after anthesis"
/lab_host="E. coli DH10B"
/clone_lib="TaE05"
/note="Vector: pSPORT-P (Invitrogen Technologies);
NotI, Site_2: MulI, mRNA obtained from wheat seeds cultivar Glenlea 5 days post-anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TaE05016F12F"
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/mol_type="mRNA"
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99.5%;
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657
                                                                                                                                                                                                                                                                597
                                                                                                                                                                                                                                                                                                                                                  477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                961 GAACATCOGCATGACAACAGGCCGCGCTCTTTCTCGGGTGTACACTCCGAGCAGAACCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Saskatchewan, Department of Computer Science 1C101 Engineering Building, 57 Campus Drive, Saskatcon, Saskatchewan, S7N 5A9, Canada Tel: 306 966 1769
Fax: 306 966 1769
Fax: 306 966 2033
Email: fgas estsecs.usask.ca
This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [18,830].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 1107)
Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Gensewein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops Unpublished (2003)
Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the region [18,830].
Plate: L58023 row: I column: 05.
Location/Qualifiers
1. .1107
                                                                                                                                                                                                                                                                                                                                                                              GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGAA 1080
                                                                                                         CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGGAGGAGGAGATAG 1200
                                                                                                                                                                                                                                                                                       gaacatecegeareacaacaeeceeeceeretteeceeretacaeteceaaecaeaacteee
                                                                                                                                                                           CGCCATGACTGGGAGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  forganism="Triticum aestivum"

/organism="Triticum aestivum"

/db xref="taxon:4565"

/db xref="taxon:4565"

/clone lib="Triticum aestivum FGAS: Library 5 GATE 7"

/clone lib="Triticum aestivum rows and developmental stages

/note="Vector: pCMV.SPORT6; Crown and developmental stages

/of spike formation in wheat cultivar Norstar. 4 mRNA

/opulations were coultivar loss constructing the library.

The first mRNA population is from lcm crown sections after 1 days of deacclimation (before

leacclimation plants were fully vernalized for 49 days).

The third is from different developmental stages of spike

formation (5 to 50mm) that still have not emerged from the

leaf (dissection required). The last is from different

developmental stages of spike and seed formation after

having emerged from the leaf (visible). First strand

synthesis in this library was done in the presence of

methylated dCTP thereby protecting from internal cleavage

with Noti."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.2%; Score 365.8; DB 99.2%; Pred. No. 3e-96; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14;
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CCCGTGCGCT

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AJ604482
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1 (bases 1 to 447)

1 (bases 1 to 447)

2 hang, D., Klueva, N., Barker, G.L.A., Wilson, I.D., Edwards, K.J., Close, T.J., Zheng, H., McCartor, K., Soares, B.M. and Nguyen, H.T. Combining expressed-sequence-tags sequencing and subtractive hybridization for rapid identification of differentially express genes under heat stress in wheat (Triticum aestivum (L.) Moench) Unpublished (2003)
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AJ604482 T07
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AJ604482.1
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum
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                                                                                                                                           GTAGCTTGTTGGTGAGCGCTCGAAAGAAAATGGACGGGCCTGGGTGTTTTGTTGTTGCAC 1260
                                                                                                                                                                                                                         CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATAG 1200
                                                                                                                                                                                                                                                          CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGCAACGGCGAGGCTGCTCTAAG 242
                                                                                                                                                                                                                                                                                           CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGGAACGGCGAGGCTGCTCCAAG 1140
                                                                                                                                                                                                                                                                                                                                GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCTGCTTGTTACAAGGCAAAGAGAGAA
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                                                                       CTGAACCCTCCTACCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG 1320
CCCGTGCGCTCAACGTGAAAAT 1342
                                             CT--ACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
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nilarity 98.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/mol_type="mRNA"
/culfivar="Mustang"
/db_xref="taxon:4565"
/clone="H12_T07_plate_9"
/tissue_type="Heat stressed whole seedlings"
/dev_stage="2_weeks_old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="T07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 361.6; DB 9
Pred. No. 3.7e-95;
0; Mismatches 4
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CCCGTGCGCTCAACGTGAACAT

442

RESULT

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SOURCE
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CD890410/c
LOCUS
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Best Local S
Matches 376
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TITLE
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                                                                                                                                                                                                                                                                                                                             1021 GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                        376;
   44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93, rue Henri Rochefort 91025
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoplante, a major 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooideae; Triticeae; Triticum.
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                       CCCGTGCGCTCAACGTGAAAAT 1342
                                                                                 CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG 1320
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 CCCGTGCGCTCAACGTGAACAT
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larity 98.4%;
Conservative
                                                           ACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /moI type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="G118114J06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="grain (118 degrees pollination)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="G118"
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Pred. No. 4.2e-95;
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a; Poales; Poaceae;
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G118114J06,
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 032 row: A column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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405 bp mRNA linear EST 03-MAY-2002
TaE15032A02F TaE15 Triticum aestivum cDNA clone TaE15032A02F, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Forward
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                                                                                        CTGAACCCTCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                                                                                                                                                                                                                                                                                                                             CTCCAGAGAGTTCGTGGATTGTGAGCGAAGCGACGGGCAACGGCGCGAGGTTGCTCCAAG
                                                                                                                                                                                                                                                                                   CGCCATGACTGGGAGGGATCGTGCCTTTTCCCCCAGATGCCAGGAGGAGCAGATGGATAG
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/dev_stage="15 days after anthesis"
/dev_stage="15 days after anthesis"
/lab_host="8. coli DHIOB"
/clome_lib="Tas15"
/clome_lib="Tas15"
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Pred. No. 8.1e-95;
0; Mismatches 6
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Triticum aestivum
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G118.127M24F010824 G118
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been 9
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Unpublished (2003)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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CCCGTGCGCTCAACGTGAAAAT 1342
                                                            CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG 1320
                                                                                                                   CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATAG 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="G118"
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/cultivar="recital"
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1 (bases 1 to 414)
Ogihara, Y. and Murai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ270799 Y. Ogihara unpublished aestivum cDNA clone whoh9k12 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856 Fax: 81-559-81-6855
BJ232268
BJ232268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed genes in Triticum aestivum Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                               GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGAAA 1080
                                                                                                                                                                                                                                  CGCCATGACTGGGAGGGGATCGTGCCTTCCCCAGATGCCAGGAGGAGGAGCAGATGGATAG
                                                                                                                                                                        CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
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/dev_stage="Feekes' scale 10.5"
/clone_lib="Y. Ogihara unpublished cDNA library,
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clone="whoh9k12"
491 bp mRNA linear Ogihara unpublished cDNA library, Wh_e
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Pred. No. 3.2e-94;
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cDNA library, Wh_oh
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ACCESSION VERSION KEYWORDS

CK153053
FQAS031606 Triticum a
mRNA sequence.
CK153053
CK153053.1 GI:389727
EST.

897 aestivum

FGAS:

mRNA linear EST 05-DEC-2 Talt2 Triticum aestivum cDNA,

EST 05-DEC-2003

GI:38972724

RESULT 11 CK153053/c LOCUS DEFINITION

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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BJ232268.1
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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Contact: Tadasu Shin-i
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Ogihara, Y. and Murai, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                          cccerececrcaacergaaaar
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   CCCGTGCGCTCAACATGAACAT
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/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="seed DPA10"
/dev_stage="Feekes' scale 11.2"
/clone_lib="Y. Ogihara unpublished cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'clone="whe11m24"
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Pred. No. 3.4e-94;
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Matches 374; Conserv
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This sequence is the direct result of the Ba
Phred (default parameters). It is the raw ba
identification of the high quality insert th
(default parameters) has been run on this se
the region [125,627].

Plate: Talt237 row: A column: 20.

Location/Qualifiers
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University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatcon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Tel: 306 966 2033
Tes: 306 966 2033
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Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum aestivum (bread wheat)
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/note="Organ: Crown; Vector: pGEM-T, SSH (suppression subtractive hybridization) cDNA library from genotype CI14106 cold hardened at 2 C for 1 day (24 H) (tester) as subtracted against genotype Norstar cold hardened at 2 c for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, driver). Nitro-pyrole anchored oligo-dT priming and non-directional cloning."
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/cultivar="Wheat line CI 14106"
/db_xref="taxon:4565"
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Expressed genes in Triticum aestivum
Unpublished (2002)
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Triticum aestivum
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BJ273375
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Location/Qualifiers
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/dev_stage="Feekes' scale 10.5"
/clone_lib="Y. Ogihara unpublished cDNA library,
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/cultivar="Chinese Spring"
/db xref="taxon:4565"
/clone="whoh16p06"
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CD934119
CD934119.1 GI:
EST.
  CD899313
G174.111021F010825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the fren plant genomics programme 'Genoplante' (http://www.genoplante.and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoplante, a major
Unpublished (2003)
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1 (bases 1 to 527)
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GR45.123A24F010723 GR45 Triticum aestivum cDNA clone
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pollination)"
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/cultivar="recital"
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/clone="GR45123A24"
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Pred. No. 5.4e-91;
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  532 bp
Triticum
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e GR45123A24,
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G174.105D15F010823 (
mRNA sequence.
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CD897227.1 GI:3267
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CD899313
CD899313.1 GI:32673641
EST
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been c
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Unpublished (2003)
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1 (bases 1 to 532)
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Triticum aestivum
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pollination)"
/clone_lib="G174"
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/cultivar="recital"
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Location/Qualifiers
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pred. No. 5.4e-91;
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Search completed: April 10, 2004, 14:06:48 Job time: 3561.4 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Eukaryota; Viiidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoplante
                                                                                                                    CCCGTGCGCT 1330
                                                                                                                                                                                                     CTGAACCCTCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATAATAACTAATAATTG 1320
                                                                                                                                                                                                                                                                                                     CCCGTGCGCT 539
                                                                                                                                                                          CTTAACCCTCCTATGTTGCACATTCCCGGGTGTTTTTGTACATATAACTAATAATTG 529
                                                                                                                                                                                                                                                          GTAGCTTGTTGGTGAGCGCTCGAAAGAAAATGGACGGGCCTGGGTGTTTGTCGTGCTGCA
                                                                                                                                                                                                                                                                                                                                             CGCCATGACTGGGAGGGATCGTGCCTCTTCCCCCTGATGCCAGGAGGATCAGATGGATAG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCAGGGAGCTCGTGGATTGTGAGCGAAGCGACGGGCAACTGCGTGAGGCTGCTCTAAG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGCTTGTTACAAGGCAAAGAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="grain (174 degrees per day after
pollination)"
/clone_lib="G174"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="G174105D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                          469
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